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NEWS 20 Simultaneous left and right truncation added to COMPENDEX,
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NEWS 22 METADEX enhancements
NEWS 23 PCTGEN now available on STN
NEWS 24 TEMA now available on STN
NEWS 25 NTIS now allows simultaneous left and right truncation
NEWS 26 PCTFUL now contains images
NEWS 27 SDI PACKAGE for monthly delivery of multifile SDI results
NEWS 28 EVENTLINE will be removed from STN
NEWS 29 PATDPFUL now available on STN
NEWS 30 Additional information for trade-named substances without
structures available in REGISTRY
NEWS 31 Display formats in DGENE enhanced
NEWS 32 MEDLINE Reload
NEWS 33 Polymer searching in REGISTRY enhanced
NEWS 34 Indexing from 1947 to 1956 added to records in CA/CAPLUS
NEWS 35 New current-awareness alert (SDI) frequency in
WPIDS/WPINDEX/WPIX
NEWS 36 RDISCLOSURE now available on STN
NEWS 37 Pharmacokinetic information and systematic chemical names
added to PHAR
NEWS 38 MEDLINE file segment of TOXCENTER reloaded
NEWS 39 Supporter information for ENCOMPAT and ENCOMPULIT updated
NEWS 40 CHEMREACT will be removed from STN
NEWS 41 Simultaneous left and right truncation added to WSCA
RAPPA enhanced with new search field, simultaneous left and
right truncation
NEWS 42 Simultaneous left and right truncation added to CBNB
NEWS 43 PASCAL enhanced with additional data

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=> file medicine, cancerlit, biosis, confsci, embase, caplus, uspatfull, pctfull, scisearch COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.42	0.42

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=> 5 more (a) 1
L1 8 FILES SEARCHED ..
L1 151 MORE (A) 1
=> dup rem 11
PROCESSING COMPLETED FOR L1
L2 100 DUP REM L1 (51 DUPLICATES REMOVED)
=> s 12 not py=>1995

'1995, NOT A VALID FIELD CODE
5 FILES SEARCHED...
L3 10 L2 NOT PY=>1995

=> d 1-10

L3 ANSWER 1 OF 10 MEDLINE
AN 80137745 MEDLINE
DN 80137745 Pubmed ID: 536396
TI (Sub-phrenic abscess: 28 cases, one death (author's trans))
AU Abcex sous-phreniques. 28 observations: 1 mort.
SO Journal de Chirurgie. (1979 Aug-Sep) 116 (8-9) 481-5.
CY Journal code: 0374754. ISSN: 0021-7697.
DT Journal: Article: (JOURNAL ARTICLE)
LA French
FS Priority Journals
EM 198005
ED Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19800514

L3 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 1983:594018 CAPLUS
DN 99:194018
TI Comment on the comment of Dr. W. Gruendler on the paper "Heats of atomization of conjugated hydrocarbons by a new semiempirical method"
AU Zivkovic, Tomislav P.
CS "Rudjer Boskovic" Inst., Zagreb, YU-41001, Yugoslavia
SO Theoretica Chimica Acta (1983), 63(5), 443-4
CODEN: TCHAMM; ISSN: 0040-5744
DT Journal
LA English

L3 ANSWER 3 OF 10 USPATFULL
AN 93:102800 USPATFULL
TI Substituted semicarbazone arthropodocides
AU Daul, John P., Wilmington, DE, United States
IN Lahm, George P., Wilmington, DE, United States
PA Marlin, Bradford S., Cochranville, PA, United States
PI E. I. Du Pont de Nemours and Company, Wilmington, DE, United States
PI (U.S. corporation)
AI US 5268388 19931207
AI US 1992-971008 19921102 (7)
AI Division of Ser. No. US 1991-689042, filed on 20 May 1991, now patented,
Pat. No. US 5182303 which is a continuation-in-part of Ser. No. US
1989-436361, filed on 13 Nov 1989, now abandoned which is a
continuation-in-part of Ser. No. US 1988-290404, filed on 27 Dec 1988,
now abandoned
DT Utility
FS Granted
LN.CNT 3597
INCL INCLM: 514/470.000
INCL: 514/080.000; 514/096.000; 514/100.000; 514/415.000; 514/443.000;
544/143.000; 546/196.000; 548/483.000; 548/111.000; 549/053.000;
549/055.000; 549/057.000; 549/466.000; 549/467.000; 549/006.000;
549/220.000
NCLM: 514/470.000
NCL: 514/080.000; 514/096.000; 514/100.000; 514/415.000; 514/443.000;
544/143.000; 546/196.000; 548/111.000; 548/483.000; 549/053.000;
549/055.000; 549/057.000; 549/466.000; 549/467.000; 549/006.000;
549/220.000
IC (5)
ICM: A61K031-34

ICS: A61K031-38; C07D367-82; C07D333-66
EXP 549/53; 549/55; 549/57; 549/466; 549/467; 549/46; 549/220; 549/113;
548/983; 544/143; 546/196; 514/80; 514/96; 514/100; 514/415; 514/443;
514/470
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 4 OF 10 USPATFULL
AN 93:7135 USPATFULL
TI Substituted semicarbazone arthropodocides
AU Daul, John P., Wilmington, DE, United States
IN Lahm, George P., Wilmington, DE, United States
PA Marlin, Bradford S., Cochranville, PA, United States
PI E. I. Du Pont de Nemours and Company, Wilmington, DE, United States
PI (U.S. corporation)
AI US 5182303 19930126
AI US 1991-689042 19910520 (7)
AI WO 1989-US5597 19891220

RLI Continuation-in-part of Ser. No. US 1989-436361, filed on 13 Nov 1989,
now abandoned which is a continuation-in-part of Ser. No. US
1988-290404, filed on 27 Dec 1988, now abandoned
DT Utility
FS Granted
LN.CNT 3598
INCL INCLM: 514/583.000
INCL: 514/530.000; 514/521.000; 514/588.000; 558/404.000; 560/028.000;
560/034.000; 564/020.000; 564/021.000; 564/036.000
NCLM: 514/583.000
NCL: 514/521.000; 514/530.000; 514/588.000; 558/404.000; 560/028.000;
560/034.000; 564/020.000; 564/021.000; 564/036.000
IC (5)
ICM: A01N047-34
ICS: A01N047-30; C07C281-12; C07C337-08
EXP 564/20; 564/21; 564/36; 514/583; 514/588
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 5 OF 10 USPATFULL
AN 89:80818 USPATFULL
TI Multicidal composition
AU Puritch, George S., Saanichton, Canada
IN Gorman, Michelle D., Victoria, Canada
PA Safer, Inc., Newton, MA, United States (U.S. corporation)
AI US 4870102 19890926
AI US 1988-182137 19880415 (7)
AI Utility
DT Utility
FS Granted
LN.CNT 286
INCL INCLM: 514/493.000
INCL: 514/560.000
NCLM: 514/493.000
NCL: 514/560.000
IC (4)
ICM: A01N055-04
ICS: 514/493; 514/560
EXP 514/493; 514/560
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 6 OF 10 USPATFULL
AN 86:59257 USPATFULL
TI Quarantine system for papaya
AU Covey, H. Melvin, Hilo, HI, United States
IN Hayes, Charles F., Kailua, HI, United States
PA The United States of America as represented by the Secretary of
Agriculture, Washington, DC, United States (U.S. government)
The University of Hawaii, Honolulu, HI, United States (U.S. corporation)

PI US 4618497 19861021
 AI US 1985-757396 19850722 (6)
 DT Utility
 FS Granted
 LN CNT 1458
 INCL INCLM: 426/233.000
 INCLM: 426/615.000; 426/521.000
 NCLM: 426/233.000
 NCLM: 426/521.000; 426/615.000
 IC [4]
 ICM: A23L001-212
 426/615; 426/438; 426/418; 426/509; 426/520; 426/231; 426/232;
 426/233; 426/521
 EXF
 L3 ANSWER 7 OF 10 USPTFULL
 AN 86:23427
 TI Pesticidal compositions
 IN Debeck, Jozeff, Oberwili, Switzerland
 Lege, John, Witterswil, Switzerland
 Bachmann, Markus, Riehen, Switzerland
 Ciba-Geigy Corporation, Ardsley, NY, United States (U.S. corporation)
 PA US 4584296 19860422
 PI US 1984-612236 19840521 (6)
 PRAI CH 1983-2942 19830530
 CH 1983-2942 19830503
 CH 1983-2944 19830503
 DT Utility
 FS Granted
 LN CNT 273
 INCL INCLM: 514/147.000
 INCLM: 514/346.000
 NCLM: 514/147.000
 NCLM: 514/346.000
 IC [4]
 ICM: A01N057-10
 ICS: A01N043-40
 EXF 424/225; 424/324; 424/263; 514/147; 514/346
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 L3 ANSWER 8 OF 10 PCTFULL COPYRIGHT 2003 Univentio
 AN 1994021905 PCTFULL ED 20020513
 TIEN IMPROVEMENTS TO COMPRESSION OR SPARK IGNITION FOUR-STROKE INTERNAL
 COMBUSTION ENGINES HAVING A VARIABLE COMPRESSION RATIO ENABLING HIGH
 SUPERCHARGING PRESSURE LEVELS
 TIFR PERFECTIONNEMENTS APPORTES AUX MOTEURS A COMBUSTION INTERNE A QUATRE
 TEMPS A RAPPORT VOLUMETRIQUE VARIABLE AUTOPRISANT DE HAUTS TAUX DE
 PRESSIONS DE SURALIMENTATION ET FONCTIONNANT PAR ALLUMAGE PAR
 COMPRESSION OU PAR ALLUMAGE COMMANDE
 IN VAN AVERMAETE, Gilbert, Charles, Henri, Louis
 PA VAN AVERMAETE, Gilbert, Lucien, Charles, Henri, Louis
 LA French
 DT Patent
 PI WO 9421905 AI 19940929
 DS W: AU BR CA CN CZ JP RU US AT BE CH DE DK ES FR GB GR IE IT LU
 MC NL PT SE
 AI 19940321
 PRAI LU 1993-88235 A 19930319
 ICM FOZB041-00
 ICS FOZD015-04
 L3 ANSWER 9 OF 10 PCTFULL COPYRIGHT 2003 Univentio
 AN 1991007382 PCTFULL ED 20020513
 TIEN SUBSTITUTED SEMICARBAZONE ARTHROPODICIDES
 TIFR ARTHROPODICIDES A BASE DE SEMICARBAZONES SUBSTITUES
 DAUB, John, Powell;

LAH, George, Philip;
 MARLIN, Bradford, Senn
 E.I. DU PONT DE NEMOURS AND COMPANY
 PA English
 LA Patent
 DT Patent
 PI WO 9107382 JP KR AI 19910530
 DS W: WO 1990-US3347 A 19900620
 AI US 1989-436,361 19891113
 PRAI US 1989-PCT/US89/05597 19891220
 ICS A01N047-34
 L3 ANSWER 10 OF 10 PCTFULL COPYRIGHT 2003 Univentio
 AN 1985002768 PCTFULL ED 20020507
 TIEN NEW THERAPEUTICAL APPLICATION OF AN INDIAN DIONE DERIVATIVE AND
 PHARMACEUTICAL COMPOSITIONS INTENDED TO SAID UTILIZATION
 TIFR NOUVELE APPLICATION THERAPEUTIQUE D'UN DERIVE DE L'INDIANE DIONE ET LES
 COMPOSITIONS PHARMACEUTIQUES DESTINEES A CET USAGE
 IN PETIBON, Guy
 PA LABORATOIRES BOUCHARD;
 PETIBON, Guy
 LA French
 DT Patent
 PI WO 8502768 AI 19850704
 DS W: AT AU BE CF CG CH CM DE DK FI FR GA GB HU JP KR LU ML MR NL
 NO SE SN TD TG US
 AI WO 1984-FR302 A 19841224
 PRAI FR 1983-83/20755 A 19831226
 ICM A61K031-12
 ICS C07C049-84
 L4 => s FADD or Fas (a) associated (a) death (a) domain
 4471 FADD OR FAS (A) ASSOCIATED (A) DEATH (A) DOMAIN
 L4 => s 14 and bind? (10a) peptid?
 L5 8 FILES SEARCHED...
 356 L4 AND BIND? (10a) PEPTID?
 L6 => dup rem 15
 PROCESSING COMPLETED FOR L5
 354 DUP REM L5 (2 DUPLICATES REMOVED)
 L6 => s 16 not py=>1995
 '1995' NOT A VALID FIELD CODE
 L7 6 FILES SEARCHED...
 0 L6 NOT PY=>1995
 =>
 => d 1-10 16
 L6 ANSWER 1 OF 354 USPTFULL
 AN 2003:159813 USPTFULL
 TI Novel molecules of the card-related protein family and uses thereof
 IN Bertin, John, Watertown, MA, UNITED STATES
 PI US 2003109428 AI 20030612
 AI US 2001-798412 AI 20010302 (9)
 RLI Continuation-in-part of Ser. No. US 2000-728260, filed on 1 Dec 2000,
 ABANDONED Continuation-in-part of Ser. No. US 2000-685791, filed on 10
 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-513904, filed
 on 25 Feb 2000, PENDING Continuation-in-part of Ser. No. US 2000-507533,
 filed on 18 Feb 2000, PENDING
 PRAI US 1999-168780P 19991201 (60)
 DT Utility

FS APPLICATION
LN CNT 5413
INCL INCLMS: 514/012.000
INCLMS: 435/006.000; 435/320.100; 435/194.000; 435/325.000; 435/069.100;
516/023.200; 530/388.260
NCL NCLMS: 514/012.000
NCLMS: 435/006.000; 435/320.100; 435/194.000; 435/325.000; 435/069.100;
536/023.200; 530/388.260
IC [7]
ICM: A61X038-17
ICS: C120001-68; C07H021-04; C12N009-12; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 2 OF 354 USPTAFULL
AN 2003:159379 USPTAFULL
TI Identification of a novel domain in the tumor necrosis factor receptor
IN family that mediates pre-ligand receptor assembly and function
Lenardo, Michael J., Bethesda, MD, UNITED STATES
Chen, Francis Ka-Ming, Silver Spring, MD, UNITED STATES
Siegel, Richard W., Washington, DC, UNITED STATES
PI US 2003:108992 A1 2003:0612
US 2002-203495 A1 2002:0809 (10)
WO 2001-US4125 2001:0209
DT Utility
FS APPLICATION
LN CNT 2206
INCL INCLMS: 435/069.100
INCLMS: 435/320.100; 435/325.000; 530/350.000; 536/023.500
NCL NCLMS: 435/069.100
NCLMS: 435/320.100; 435/325.000; 530/350.000; 536/023.500
IC [7]
ICM: C07K014-715
ICS: C07H021-04; C12P021-02; C12N005-06

L6 ANSWER 3 OF 354 USPTAFULL
AN 2003:153330 USPTAFULL
TI Secreted and transmembrane polypeptides and nucleic acids encoding the
IN same
Ashkenazi, Avi J., San Mateo, CA, UNITED STATES
Baker, Kevin P., Darnestown, MD, UNITED STATES
Botstein, David, Belmont, CA, UNITED STATES
Desnoyers, Luc, San Francisco, CA, UNITED STATES
Eaton, Dan L., San Rafael, CA, UNITED STATES
Ferrara, Napoleone, San Francisco, CA, UNITED STATES
Filaroff, Ellen, San Francisco, CA, UNITED STATES
Fong, Sherman, Alameda, CA, UNITED STATES
Gao, Wei-Qiang, Palo Alto, CA, UNITED STATES
Gerber, Hanspeter, San Francisco, CA, UNITED STATES
Gertsen, Mary E., San Mateo, CA, UNITED STATES
Goddard, Audrey, San Francisco, CA, UNITED STATES
Goddard, Paul J., Burlingame, CA, UNITED STATES
Grimaldi, J. Christopher, San Francisco, CA, UNITED STATES
Gurney, Austin L., Belmont, CA, UNITED STATES
Hillman, Kenneth J., San Francisco, CA, UNITED STATES
Kiljavin, Ivar J., Lafayette, CA, UNITED STATES
Kuo, Sophia S., San Francisco, CA, UNITED STATES
Napier, Mary A., Hillsborough, CA, UNITED STATES
Pan, James, Belmont, CA, UNITED STATES
Paoni, Nicholas F., Belmont, CA, UNITED STATES
Roy, Margaret Ann, San Francisco, CA, UNITED STATES
Shelton, David L., Oakland, CA, UNITED STATES
Stewart, Timothy A., San Francisco, CA, UNITED STATES
Tunas, Daniel, Orinda, CA, UNITED STATES
Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
Wood, William I., Hillsborough, CA, UNITED STATES

PA Genentech, Inc. (U.S. corporation)
PI US 2003:104998 A1 2003:10605
AI US 2001-978643 A1 2001:1016 (9)
RLI Continuation of Ser. No. US 1998-40220, filed on 17 Mar 1998, GRANTED,
Pat. No. US 6391311 Continuation of Ser. No. US 1998-105413, filed on 26
Jun 1998, ABANDONED Continuation of Ser. No. US 1998-168978, filed on 7
Oct 1998, ABANDONED Continuation of Ser. No. US 1998-184216, filed on 2
Nov 1998, ABANDONED Continuation of Ser. No. US 1998-187368, filed on 6
Nov 1998, PENDING Continuation of Ser. No. US 1998-202054, filed on 7
Dec 1998, PENDING Continuation of Ser. No. US 1998-218517, filed on 22
Dec 1998, ABANDONED Continuation of Ser. No. US 1999-254465, filed on 5
Mar 1999, GRANTED, Pat. No. US 6410708 Continuation of Ser. No. US
1999-265686, filed on 10 Mar 1999, GRANTED, Pat. No. US 6455283
Continuation of Ser. No. US 1999-267213, filed on 12 Mar 1999, ABANDONED
Continuation of Ser. No. US 1999-284291, filed on 12 Apr 1999, ABANDONED
Continuation of Ser. No. US 1999-311832, filed on 14 May 1999, PENDING
Continuation of Ser. No. US 1999-318137, PENDING Continuation of Ser. No. US
1999-380138, filed on 25 Aug 1999, ABANDONED Continuation of Ser. No. US
1999-380142, filed on 25 Aug 1999, ABANDONED Continuation of Ser. No. US
2000-709238, filed on 8 Nov 2000, ABANDONED Continuation of Ser. No. US
2000-723749, filed on 27 Nov 2000, PENDING Continuation of Ser. No. US
2000-747259, filed on 20 Dec 2000, PENDING Continuation of Ser. No. US
2001-816744, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US
2001-816920, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US
2001-854280, filed on 10 May 2001, PENDING Continuation of Ser. No. US
2001-854208, filed on 10 May 2001, PENDING Continuation of Ser. No. US
2001-872035, filed on 1 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-874503, filed on 5 Jun 2001, PENDING Continuation of Ser. No. US
2001-882636, filed on 14 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-886342, filed on 19 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-918585, filed on 30 Jul 2001, PENDING
WO 1998-US21141 1998:1007
WO 1998-US24855 1998:1120
WO 1999-US106 1999:0105
WO 1999-US5028 1999:0308
WO 1999-US5190 1999:0310
WO 1999-US10733 1999:0514
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WO 2001-US17092 2001:0525

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MO 2001-US21735 20010709
US 1997-62250P 19971017 (60)
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US 1998-94651P 19980730 (60)
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US 1999-146222P 19990728 (60)
US 1999-162506P 19991029 (60)

DT
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IN.CNT 21741
INCL INCLM: 514/012.000
INCLM: 530/388.100; 536/023.200; 435/006.000; 435/069.100;
INCLM: 435/007.100; 435/325.000; 435/320.100
NCL NCIM: 514/012.000
NCLM: 530/350.000; 530/388.100; 536/023.200; 435/006.000; 435/069.100;
NCLM: 435/007.100; 435/325.000; 435/320.100
IC [7]
ICM: A61K038-17
ICS: C12Q001-68; G01N033-53; C07H021-04; C12P021-02
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L6 ANSWER 4 OF 354 USPATFULL
AN 2003:152892 USPATFULL

TI Secreted and transmembrane polypeptides and nucleic acids encoding the same

IN Ashkenazi, Avi J., San Mateo, CA, UNITED STATES
 Baker, Kevin P., Darnestown, MD, UNITED STATES
 Botstein, David A., Belmont, CA, UNITED STATES
 Desnoyers, Luc, San Francisco, CA, UNITED STATES
 Eaton, Dan L., San Rafael, CA, UNITED STATES
 Ferrara, Napoleone, San Francisco, CA, UNITED STATES
 Fong, Sherman, Alameda, CA, UNITED STATES
 Gao, Wei-Qiang, Palo Alto, CA, UNITED STATES
 Gerber, Hanspeter, San Francisco, CA, UNITED STATES
 Gerltsen, Mary E., San Mateo, CA, UNITED STATES
 Goddard, Audrey, San Francisco, CA, UNITED STATES
 Godowski, Paul J., Hillsborough, CA, UNITED STATES
 Gurney, Austin J., Belmont, CA, UNITED STATES
 Kijavini, Ivar J., Lafayette, CA, UNITED STATES
 Mather, Jennie P., Millbrae, CA, UNITED STATES
 Napier, Mary A., Hillsborough, CA, UNITED STATES
 Pan, James, Belmont, CA, UNITED STATES
 Paoni, Nicholas F., Belmont, CA, UNITED STATES
 Roy, Margaret Ann, San Francisco, CA, UNITED STATES
 Stewart, Timothy A., San Francisco, CA, UNITED STATES
 Tumas, Daniel, Orinda, CA, UNITED STATES
 Watanabe, Colin K., Moraga, CA, UNITED STATES
 Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
 Wood, William I., Hillsborough, CA, UNITED STATES
 Zhang, Zemin, Foster City, CA, UNITED STATES
 Genentech Inc. (U.S. corporation)

PA US 2003104558 AI 20030605
 PI US 2002-226739 AI 20020823 (10)
 RLI Continuation of Ser. No. US 2001-2796, filed on 15 Nov 2001, PENDING
 PRAI Continuation of Ser. No. US 2000-154042, filed on 22 May 2000, PENDING

PA US 1999-US20111 19990901
 PI US 1999-US20594 19990908
 RLI US 1999-US21090 19990915
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 PI US 1999-US28313 19991130
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 RLI US 2001-US21735 20010709
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 INCL INCL: 435/069.100
 INCL: 435/183.000; 435/320.100; 435/325.000; 530/350.000; 536/023.200
 NCL NCLM: 435/069.100
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 ICM: C12P021-02
 ICS: C12N005-06; C07K014-435; C07H021-04; C12N009-00
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 5 OF 354 USPATFULL
 AN 2003152870 USPATFULL
 TI Secreted and transmembrane polypeptides and nucleic acids encoding the same

IN Ashkenazi, Avi J., San Mateo, CA, UNITED STATES
 Baker, Kevin P., Darnestown, MD, UNITED STATES
 Botstein, David, Belmont, CA, UNITED STATES
 Desnoyers, Luc, San Francisco, CA, UNITED STATES
 Eaton, Dan L., San Rafael, CA, UNITED STATES
 Ferrara, Napoleone, San Francisco, CA, UNITED STATES
 Fong, Sherman, Alameda, CA, UNITED STATES
 Gao, Wei-Qiang, Palo Alto, CA, UNITED STATES
 Gerber, Hanspeter, San Francisco, CA, UNITED STATES
 Gerltsen, Mary E., San Mateo, CA, UNITED STATES
 Goddard, Audrey, San Francisco, CA, UNITED STATES
 Godowski, Paul J., Burlingame, CA, UNITED STATES
 Girmaidi, J. Christopher, San Francisco, CA, UNITED STATES
 Gurney, Austin J., Belmont, CA, UNITED STATES
 Hillan, Kenneth J., San Francisco, CA, UNITED STATES
 Kijavini, Ivar J., Lafayette, CA, UNITED STATES
 Kuo, Sophia S., San Francisco, CA, UNITED STATES
 Napier, Mary A., Hillsborough, CA, UNITED STATES
 Pan, James, Belmont, CA, UNITED STATES
 Paoni, Nicholas F., Belmont, CA, UNITED STATES
 Roy, Margaret Ann, San Francisco, CA, UNITED STATES
 Shelton, David L., Oakland, CA, UNITED STATES
 Stewart, Timothy A., San Francisco, CA, UNITED STATES
 Tumas, Daniel, Orinda, CA, UNITED STATES
 Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
 Wood, William I., Hillsborough, CA, UNITED STATES
 Genentech Inc. (U.S. corporation)

PA US 2003104536 AI 20030605
 PI US 2001-16709 AI 20010119 (10)
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 PI US 2000-US219 20000105
 RLI US 2000-US277 20000106
 PRAI US 2000-US376 20000106

PA Tumas, Daniel, Orinda, CA, UNITED STATES
PI Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
AI Wood, William I., Hillsborough, CA, UNITED STATES
RLI Genetech, Inc. (U.S. corporation)
US 20003056744 AI 200030522
US 2002-978187 AI 20020128 (9)

Continuation of Ser. No. US 2001-918585, filed on 30 Jul 2001, PENDING
Pat. No. US 6391311 Continuation of Ser. No. US 1998-40220, filed on 17 Mar 1998, GRANTED
Jun 1998, ABANDONED Continuation of Ser. No. US 1998-105413, filed on 26
Oct 1998, ABANDONED Continuation of Ser. No. US 1998-168378, filed on 7
Nov 1998, ABANDONED Continuation of Ser. No. US 1998-184216, filed on 2
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Mar 1999, GRANTED, Pat. No. US 6410708 Continuation of Ser. No. US
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Continuation of Ser. No. US 1999-284291, filed on 12 Apr 1999, ABANDONED
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1999-380138, filed on 25 Aug 1999, ABANDONED Continuation of Ser. No. US
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2000-723749, filed on 8 Nov 2000, ABANDONED Continuation of Ser. No. US
2000-747259, filed on 27 Nov 2000, PENDING Continuation of Ser. No. US
2001-816744, filed on 20 Dec 2000, PENDING Continuation of Ser. No. US
2001-816720, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US
2001-854280, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US
2001-854280, filed on 10 May 2001, PENDING Continuation of Ser. No. US
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2001-874503, filed on 5 Jun 2001, PENDING Continuation of Ser. No. US
2001-882636, filed on 19 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-886342, filed on 14 Jun 2001, ABANDONED

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US 1999-141037P 19990623 (60)
US 1999-142680P 19990707 (60)
US 1999-145698P 19990726 (60)
US 1999-146222P 19990728 (60)
US 1999-162506P 19991029 (60)

DT Utility
FS APPLICATION
LN.CNT 21776
INCL INCLM: 514/012.000; 435/320.100; 435/183.000; 435/325.000; 530/350.000;
INCLM: 435/069.100; 435/320.100; 435/183.000; 435/325.000; 530/350.000;
NCLM: 514/012.000
NCLM: 514/012.000; 435/320.100; 435/183.000; 435/325.000; 530/350.000;
NCLM: 536/023.200
IC (7)
ICM: A61K038.17
ICS: C12P021-02; C12N005-06; C07H014-435; C07H021-04; C12N009-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 10 OF 354 USPATFUL
AN 2003:140406 USPATFUL
TI Human CDNs and proteins and uses thereof
IN Bejanin, Stephane, Paris, FRANCE
Tanaka, Hiroaki, Antony, FRANCE
PA GENSET, S.A., Paris, FRANCE, 75008 (non-U.S. corporation)
PI US 2003096247 AI 20030522
PI US 2001986 AI 20011114 (10)
AI US 2001986 AI 20011114 (10)
RLI Division of Ser. No. US 2001-924340, filed on 6 Aug 2001, PENDING
PRAI WO 2001-181715 20010806
US 2001-305456P 20010713 (60)
US 2001-302277P 20010629 (60)
US 2001-298698P 20010615 (60)
US 2001-293574P 20010525 (60)

DT Utility
FS APPLICATION
LN.CNT 2566
INCL INCLM: 435/006.000
INCLM: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
INCLM: 435/023.200; 800/008.000
NCLM: 435/006.000
NCLM: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
IC (7)
ICM: C12N001-68
ICS: A01K067-00; C07H021-04; C12N009-00; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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L6 ANSWER 10 OF 354 USPATFUL
DETD a contiguous surface of the native conformation of a polypeptide of the present application. Additionally, the antibody is capable of binding a nonlinear epitope presented by a synthetic peptide designed to mimic a contiguous surface of the native conformation of a polypeptide of a sequence selected from the group.
DETD use in caspase-dependent cell death including incubation of carcinoma cells with compositions comprising polypeptides of preferred sequences comprising RLMGRDENKIMDEDES and PADD DED-related domains as described in Eberstadt, et al., Nature, 392:941-945, 1998, and Hackam, et al., J.Biol.Chem. 275:41299-41308, 2000, which disclosures are hereby.
DETD effector domain RLMGRDENKIMDEDES, and the death effector domain of the huntingtin-interacting protein (HIP-1), conserved among related sequences with the consensus peptide SSYRLRLILISELSELEVLFLCNDIPKRLKLTALDLSALEEGGLISEDNLSLAE LYLRLRLDLRLRFG for competitive binding studies with wild-type huntingtin and the disease-causing mutant. By contacting polypeptides of the invention with wt- and mt- (glutamine-rich) huntingtin.
DETD sulfated glycosaminoglycans covalently bound to core protein. The ability to bind heparin-like moieties includes RFGs within the more encompassing Heparin Binding Growth Factor (HBGF) superfamily; of peptide growth factors. Additionally, RFGs bind the cysteine-rich FGF-R (CFR), an integral single transmembrane protein in a mutually exclusive manner with respect to the other RFGs.
DETD amino acid protein that is highly homologous to the amino-terminal "prepro" region of procaspase-9. The "pre" region represents a signal peptide while the "pro" region inhibits carboxypeptidase enzyme activity by binding to the active site of the enzyme before being proteolytically removed. Proteolytic cleavage of procaspase-9 results in formation of mature.

DETD 84/03564, published on Sep. 13, 1984, and incorporated herein by reference in its entirety, may be used to screen for peptide compounds which demonstrate binding affinity for B2RP-R2 polypeptides or fragments thereof. In another embodiment, competitive drug screening assays using neutralizing antibodies specifically compete with.

DETD G protein-binding amino acid sequence DRP is found near the first transmembrane region of AAR. The extracellular portion of AAR binds to ligands that include amyloidogenic peptides. Ligand binding leads to apoptosis for the AAR-expressing cell. AAR has biological activities that comprise binding G protein components and ligands such as amyloidogenic peptides.

DETD is contacted with a cell in an amount effective to induce apoptosis of the cell. Preferred AAR ligands are compounds that bind specifically to AAR and cause apoptosis in the cell expressing AAR. Further preferred AAR ligands include AAR-specific antibodies. Preferred AAR-specific.

DETD [1227] The amino-terminus of AAR is capable of binding to ligands such as amyloidogenic peptides (i.e., the beta-amyloid peptide associated with Alzheimer's disease, Amyloid Precursor Like Proteins (APLP) 1 and 2, immunoglobulin light chain, prealbumin).

DETD 84/03564, published on Sep. 13, 1984, and incorporated herein by reference in its entirety, may be used to screen for peptide compounds which demonstrate binding affinity for, or the ability to modulate, the NBHSD2, or biologically active fragments thereof in another embodiment, competitive drug screening [1597] For the purpose of the present invention, a ligand means a molecule, such as a protein, a peptide, an antibody or any synthetic chemical compound capable of binding to a GENSER protein or one of its fragments or variants or to modulate the expression of the polynucleotide coding.

DETD [1606] Alternatively, peptides, drugs or small molecules which bind to polypeptide of the present invention may be identified in competition experiments. In such assays, the GENSER protein, or a

DETD or portions thereof. Alternatively, the inhibitor can be an agent other than an antibody (e.g., small organic molecule, protein or peptide) which binds the GENSER polypeptide and blocks its activity. For example, the inhibitor can be an agent which mimics the GENSER polypeptide.

DETD Identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

=> d his

(FILE 'HOME' ENTERED AT 10:10:43 ON 19 JUN 2003)

FILE 'MEDLINE, CANCERLIT, BIOSIS, CONFSCI, EMBASE, CAPLUS, USPATFULL, PCTFULL, SCISEARCH' ENTERED AT 10:11:35 ON 19 JUN 2003

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L2 100 DUP REM L1 (51 DUPLICATES REMOVED)

L3 10 S L2 NOT PY=>1995

L4 4471 S FADD OR FAS (A) ASSOCIATED (A) DEATH (A) DOMAIN

L5 356 S L4 AND BIND (10A) PEPTID?

L6 354 DUP REM L5 (2 DUPLICATES REMOVED)

L7 0 S L6 NOT PY=>1995

=> S L6 not PY=>1996

'1996' NOT A VALID FIELD CODE

L8 6 FILES SEARCHED...

=> 0 L6 NOT PY=>1996

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---Logging off of STN---

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Executing the logoff script...

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COST IN U.S. DOLLARS

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 10:36:11 ON 19 JUN 2003

SINCE FILE	TOTAL
ENTRY	73.67
SESSION	74.09

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:42:06 ; Search time 32 seconds
(without alignments)
1648.377 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
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Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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20	8	3.1	639	10	Q9C884	Q9C884 arabidopsis
21	8	3.1	636	10	Q9L629	Q9L629 arabidopsis
22	8	3.1	681	2	Q93M24	Q93M24 cornebacte
23	8	3.1	683	2	Q46072	Q46072 cornebacte
24	8	3.1	751	11	Q9R1X1	Q9R1X1 mus musculu
25	8	3.1	751	11	Q9R207	Q9R207 mus musculu
26	8	3.1	821	2	Q8VPM9	Q8VPM9 micrococcu
27	8	3.1	1109	10	Q8S750	Q8S750 oryza sativ
28	8	3.1	1209	10	Q94FG7	Q94FG7 chlamydomon
29	8	3.1	1787	10	Q9M4X9	Q9M4X9 chlamydomon
30	8	3.1	2166	5	Q9YK42	Q9YK42 drosophila
31	8	3.1	2639	5	Q76786	Q76786 antheraea p
32	8	3.1	2655	5	Q964F4	Q964F4 antheraea y
33	8	3.1	2910	5	Q26008	Q26008 plasmodium
34	8	3.1	3763	5	Q8T2A1	Q8T2A1 dictyostell
35	8	2.7	48	5	Q9VN62	Q9VN62 drosophila
36	8	2.7	63	5	Q9VTH6	Q9VTH6 drosophila
37	7	2.7	77	16	Q05451	Q05451 mycobacteri
38	7	2.7	92	11	Q9CTP6	Q9CTP6 mus musculu
39	7	2.7	95	6	Q97516	Q97516 gorilla gor
40	7	2.7	95	6	Q97519	Q97519 pongo pygma
41	7	2.7	95	6	Q97520	Q97520 pongo pygma
42	7	2.7	102	17	Q8U208	Q8U208 pyrococcus
43	7	2.7	105	10	Q8S2C9	Q8S2C9 oryza sativ
44	7	2.7	106	16	Q34418	Q34418 bacillus su
45	7	2.7	111	3	Q9HGVO	Q9HGVO aspergillus

ALIGNMENTS

RESULT 1
Q8R2E7 PRELIMINARY; PRT; 208 AA.

AC Q8R2E7; Q8R2E7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Fas death domain associated protein.
OS FADD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
PP [1]
PP SEQUENCE FROM N.A.
PP STRAIN=SPRAGUE-DAWLEY; TISSUE=ISCHEMIC BRAIN;
PP Neame S.; (Apr-2002) to the EMBL/GenBank/DBJ databases;
PP Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases;
PP [2]
PP SEQUENCE FROM N.A.
PP STRAIN=SPRAGUE-DAWLEY; TISSUE=ISCHEMIC BRAIN;
PP Spadoni C.G.;
PP "Identification of neuronal caspases and involvement of death domain
PP proteins in neuronal apoptosis."
PP Theiss (2001), University of London, London, United Kingdom.
PP EMBL; AJ441127; CAD29628.1;
SQ SEQUENCE 208 AA; 23124 MW; ABA305406137CDB CRC64;

Query Match 5.9%; Score 15; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLKRVSGGLDLS 95
DB 33 KRKLKRVSGGLDLS 47
RESULT 2
Q9RDQ8

ID 09R08 PRELIMINARY; PRT; 295 AA.
 AC 09R08
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Hypothetical protein SC02376.
 GN SC02376 OR SCA47.04.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2)/M145;
 RA Beutley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbitts E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL:AL133423; CAB62708.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 295 AA; 31729 MW; FE8B3A677A451189 CRC64;

Query Match 3.5%; Score 9; DB 16; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 140
 DB 197 AGAAGAA 205

RESULT 3
 ID 097518 PRELIMINARY; PRT; 99 AA.
 AC 097518;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Dopamine D4 receptor (Fragment).
 GN DRD4.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20215006; PubMed=10750051;
 RA Seaman M.I., Chang F.M., Delnard A.S., Quiñones A.T., Kidd K.R.,
 RT "Evolution of exon 1 of the dopamine D4 receptor (DRD4) gene in
 RT primates";
 RL J. Exp. Zool. 288:32-38(2000).
 DR EMBL:AF010298; AAC67226.1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2.1.
 KW Receptor.
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 9535 MW; DACED9750184BC47 CRC64;

Query Match 3.1%; Score 8; DB 6; Length 99;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 20 AGAAGAA 27

RESULT 4
 ID 09Y9X0 PRELIMINARY; PRT; 118 AA.
 AC 09Y9X0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Hypothetical protein APE2169.
 GN APE2169.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankel A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1";
 RL DNA Res. 6:83-101(1999).
 DR EMBL:AF000063; BAA81180.1; -
 KW Hypothetical protein, Complete proteome.
 SQ SEQUENCE 118 AA; 11827 MW; 68F7241C9D7678 CRC64;

Query Match 3.1%; Score 8; DB 17; Length 118;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 57 AGAAGAA 64

RESULT 5
 ID 09RV6 PRELIMINARY; PRT; 224 AA.
 AC 09RV6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Hypothetical protein DR0915.
 GN DR0915.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson J.L.,
 RA Morfitt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Yamahirovan J.J., Lam P., McDonald L., Usterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioreistant bacterium Deinococcus
 RT radiodurans R1";
 RL Science 286:1571-1577(1999).
 DR EMBL:AE001944; AAP10496.1; -
 DR TIGR: DR0915;
 KW Hypothetical protein, Complete proteome.

SO SEQUENCE 224 AA; 21492 MW; DC4D770547E24AED CRC64;

Query Match 3.18; Score 8; DB 16; Length 224;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 173 AGAAGAA 180

RESULT 6

OY 09K191 PRELIMINARY; PRT; 265 AA.

AC 09K191; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

OS Bacillus anthracis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OX NCBI_TaxID=1392;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=83;

RA MEDLINE=20327579; PubMed-10869077;

RT Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Kelm P.;

RL "vrb, a hypervariable open reading frame in bacillus anthracis.";

DR J. Bacteriol. 182:3989-3997(2000).

DR EMBL; AF338885; AAF6199.1;

DR HSP; P13231; HCE.

DR InterPro; IPR002395; KINNOGEN.

DR PRINTS; PR00334; KINNOGEN.

FT VARIANT 75 75 A -> T.

FT VARIANT 123 123 H -> O.

SO SEQUENCE 265 AA; 27775 MW; 8C70F8E508D28E47 CRC64;

Query Match 3.18; Score 8; DB 2; Length 265;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 244 AGAAGAA 251

RESULT 7

OY 030371 PRELIMINARY; PRT; 291 AA.

AC 030371; 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

RA Stintzi A., Johnson Z., Stonehouse M., Ochsen U., Meyer J.M.,

RT "The pvc gene cluster of Pseudomonas aeruginosa: role in synthesis of

the pyoverdine chromophore and regulation by PtxR and pvdS.";

RL J. Bacteriol. 181:4118-4124(1999).

DR EMBL; AF002222; AAC21672.1;

SO SEQUENCE 291 AA; 33165 MW; A96B2B449132C81 CRC64;

Query Match 3.18; Score 8; DB 2; Length 291;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRR 120

DB 224 ELASLRR 231

RESULT 8

OY 09I114 PRELIMINARY; PRT; 291 AA.

AC 09I114; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PA01;

RA MEDLINE=20437337; PubMed-10984043;

RT Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,

RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,

RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an

opportunistic pathogen.";

RL Nature 406:959-964(2000).

DR EMBL; AE004651; AAG05643.1;

DR Complete proteome.

SO SEQUENCE 291 AA; 33137 MW; 1D2E02B01850BD87 CRC64;

Query Match 3.18; Score 8; DB 16; Length 291;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRR 120

DB 224 ELASLRR 231

RESULT 9

OY 09K187 PRELIMINARY; PRT; 294 AA.

AC 09K187; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

OS Bacillus cereus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OX NCBI_TaxID=1396;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 43881;

RA MEDLINE=20327579; PubMed-10869077;

RA Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Keim P.;
 RT "vrb, a hypervariable open reading frame in bacillus anthracis."
 RL J. Bacteriol. 182:3989-3997(2000).
 DR EMBL: AF238888; AAF86203.1;
 DR InterPro: IPR002395; Kintinogen.
 DR PRINTS: PR00334; KININOGEN.
 FT NON_TER 1
 SO SEQUENCE 294 AA; 30753 MW; C05B7B37FE2E395C CRC64;

Query Match 3.1%; Score 8; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 273 AGAAGAA 280

RESULT 10

ID 09K189 PRELIMINARY; PRT; 296 AA.
 AC 09K189;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Putative vrb (Fragment).
 GN VRRB.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AVCC 11778;
 RX MEDLINE=20327579; PubMed=10869077;
 RA Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Keim P.;
 RT "vrb, a hypervariable open reading frame in bacillus anthracis."
 RL J. Bacteriol. 182:3989-3997(2000).
 DR EMBL: AF238888; AAF86203.1;
 DR InterPro: IPR002395; Kintinogen.
 DR PRINTS: PR00334; KININOGEN.
 FT NON_TER 1
 SO SEQUENCE 296 AA; 31360 MW; 332D6B6CE0A57A5A CRC64;

Query Match 3.1%; Score 8; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 273 AGAAGAA 282

RESULT 11

ID 08W0M6 PRELIMINARY; PRT; 301 AA.
 AC 08W0M6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative myb-related transcription factor.
 GN P0681B1.6 OR B1085F01.21.
 OS Oryza sativa (Rice), and
 OY Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Elmhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530; 39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa niponbare(GA3) genomic DNA, chromosome 1, PAC

RT clone: P0681B1."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBD databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa niponbare(GA3) genomic DNA, chromosome 1, BAC
 clone: B1085F01."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBD databases.
 DR EMBL: AF003022; BAB78640.1;
 DR EMBL: AF003330; BAB89885.1;
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR InterPro: IPR001878; ZnF_CCHC.
 DR Pfam: PF00249; myb_DNA_binding; 1.
 DR Pfam: PF00998; ZnF_CCHC; 1.
 DR SMART: SM00395; SANT; 1.
 DR PROSITE: PS50090; MYB_3; 1.
 SO SEQUENCE 301 AA; 31281 MW; 26B8364B7A6FB87 CRC64;

Query Match 3.1%; Score 8; DB 10; Length 301;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 AAGAGG 141
 DB 80 AAGAGG 87

RESULT 12

ID 09V55 PRELIMINARY; PRT; 316 AA.
 AC 09V55;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG5573 protein.
 GN CG5573.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang C., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Aspray A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burlis R.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostali M., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shne B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003525; AAF9366.1; -
 DR Flybase: FBgn0036701; CG6573.
 SQ SEQUENCE 316 AA; 32745 MW; D99DCD8CBA14CB1 CRC64;

Query Match 3.1%; Score 8; DB 5; Length 316;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 AGAAGAPG 141
 DB 179 AAGAGAPG 186

RESULT 13
 ID 09RUAB PRELIMINARY; PRT; 316 AA.
 AC 09RUAB:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein DRI483.
 GN DRI483
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RI
 RX MEDLINE=20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Yamathavan J.J., Lam P., McDonald L., Otterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.,
 RT "Genome sequence of the radioresistant bacterium *Deinococcus*
 RT radiodurans RI."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001993; AAF11061.1; -
 DR TIGR: DRI483; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 316 AA; 32287 MW; C7E37F30028D53CA CRC64;

Query Match 3.1%; Score 8; DB 16; Length 316;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 138 AGAAGAA 145

RESULT 14
 ID 065254 PRELIMINARY; PRT; 396 AA.
 AC 065254:
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 43.9 kDa protein.

GN F21E10.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eutariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Davidson S., Rohlfing T., David M., O'Brian D.,
 RT "The sequence of *A. thaliana* F21E10."
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Washu;
 RT "The *A. thaliana* Genome Sequencing Project."
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Waterston R.,
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Wilson R.,
 RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF058914; AAC13598.1; -
 DR InterPro: IPR005178; DUF300.
 DR Pfam: PF03619; DUF300; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 396 AA; 43939 MW; 61EA801F1E2C1EF1 CRC64;

Query Match 3.1%; Score 8; DB 10; Length 396;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 SVSSSLSS 65
 DB 328 SVSSSLSS 335

RESULT 15
 ID 08RDY8 PRELIMINARY; PRT; 400 AA.
 AC 08RDY8:
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ABC transporter permease protein.
 GN FNI353.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 25586;
 RX MEDLINE=2186394; PubMed-1189109;
 RA Kapatal V., Anderson I., Ivanova N., Resnik G., Los T., Lykdis A.,
 RA Bhattacharya A., Bartan A., Gardner W., Grecklin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fongstein M., Kyriades N., Overbeek R.,
 RT "Genome sequence and analysis of the oral bacterium *Fusobacterium*
 RT nucleatum strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL: AE010640; AAL95549.1; -
 KW Complete proteome.
 SQ SEQUENCE 400 AA; 44260 MW; 16674867AAC35157 CRC64;

Query Match 3.1%; Score 8; DB 16; Length 400;
 Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 DTKIDSIE 178
|||||||

Db 223 DTKIDSIE 230

Search completed: June 19, 2003, 10:46:29
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:39:31 ; Search time 11 Seconds
(without alignments)
965.267 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VMDPFCRGGGILGRLGRK.....RSGAMSPMSNDASTSEAS 256

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	68.8	208	FADD_HUMAN	Q13158 homo sapien
2	15	5.9	205	FADD_MOUSE	O61160 mus musculu
3	9	3.5	681	YDHE_SCHPO	G92359 schistosacch
4	8	3.1	82	MT21_ORYSA	P94029 oryza sativ
5	8	3.1	128	RL7_THREMA	P29396 thernotoga
6	8	3.1	174	PER_ACEME	P12347 acetabulari
7	8	3.1	258	YNM8_YEAST	P53862 saccharomyc
8	8	3.1	429	OCRA_MYCTU	Q10387 mycobacteri
9	8	3.1	468	IL9R_MOUSE	O01114 mus musculu
10	8	3.1	499	NPXR_HUMAN	O95502 homo sapien
11	8	3.1	683	PTNA_CORGU	Q46072 corynebacte
12	8	3.1	930	PRGR_RABIT	P06186 coryctolagus
13	8	3.1	1698	41_DROME	G9V8C9 drosophila
14	8	3.1	1887	FAS2_YEAST	P19097 s fatty aci
15	7	2.7	61	OM06_YEAST	P33448 saccharomyc
16	7	2.7	73	XO55_NPYAC	P14458 altosgrapha
17	7	2.7	121	RL7_CLOPE	O6XHT7 clostridium
18	7	2.7	124	YBF3_YEAST	P81190 saccharomyc
19	7	2.7	128	RL7_AOUAE	O67761 aquilex aeo
20	7	2.7	130	RL7_MYCTU	P37381 mycobacteri
21	7	2.7	158	RSD_ECOLI	P31690 escherichia
22	7	2.7	185	LPRB_MYCTU	Q11045 mycobacteri
23	7	2.7	193	HS72_CANAL	P46387 candida alb
24	7	2.7	198	YH13_YEAST	P38896 saccharomyc
25	7	2.7	202	NADD_CLOPE	O6X114 clostridium
26	7	2.7	204	RR42_HUMAN	P17082 homo sapien
27	7	2.7	216	PENL_XENLA	P07194 xenopus lae
28	7	2.7	219	YIAD_ECOLI	P37665 escherichia
29	7	2.7	245	HIS4_YERPE	O6Z1X5 yersinia pe
30	7	2.7	255	DAB2_YEAST	P21705 saccharomyc
31	7	2.7	261	PRP2_MOUSE	P05147 mus musculu
32	7	2.7	262	PENK_XENLA	P01212 xenopus lae
33	7	2.7	265	RL7A_FUGRU	O57592 fugu rubrip

34	7	2.7	296	1	PRP3_MOUSE	P05143 mus musculu
35	7	2.7	317	1	ISPE_ANASP	O8V561 anabena sp
36	7	2.7	327	1	PXA2_SALTI	P58716 salmonella
37	7	2.7	327	1	PXA2_SALTY	P58716 salmonella
38	7	2.7	331	1	MACS_BOVIN	P12624 bos taurus
39	7	2.7	345	1	OGG1_RAT	O70249 rattus norv
40	7	2.7	347	1	CTPT_CAEEL	P49583 caenorhabdi
41	7	2.7	361	1	HYPB_ALCEU	P31902 alcaigenes
42	7	2.7	367	1	PROB_MYCLE	O9CB25 mycobacteri
43	7	2.7	373	1	YLU2_PICAN	P34735 picula angu
44	7	2.7	376	1	PROB_MYCTU	P71910 mycobacteri
45	7	2.7	378	1	DNJ2_MYCLE	Q49762 mycobacteri

ALIGNMENTS

RESULT 1	ID	FADD_HUMAN	STANDARD:	PRT:	208 AA.
AC	Q13158	Q14866			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	FADD protein (FAS-associating death domain-containing protein)				
DE	(Mediator of receptor induced toxicity).				
GN	FADD OR MORT1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.				
RC	TISSUE=Umbilical vein endothelial cells;				
RX	MEDLINE=95277837; PubMed=7538907;				
RA	Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;				
RT	"FADD, a novel death domain-containing protein, interacts with the				
RT	death domain of Fas and initiates apoptosis.";				
RL	Cell 81:505-512(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95229578; PubMed=7536190;				
RA	Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,				
RT	Wallach D.;				
RT	"A novel protein that interacts with the death domain of Fas/APo1				
RL	J. Biol. Chem. 270:7795-7798(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				
RT	Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	STRUCTURE BY NMR OF 1-83.				
RX	MEDLINE=98241233; PubMed=9582077;				
RA	Ederstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,				
RT	Lenardo M.J., Fesik S.W.;				
RT	"NMR structure and mutagenesis of the FADD (Mort1) death-effector				
RL	domain.";				
RL	Nature 392:941-945(1998).				
CC	-I- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR				
CC	CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNF-R1 RECEPTORS. THE				
CC	RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX				
CC	(DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8				
CC	INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC				
CC	STEIN PROTEASES) MEDIATING APOPTOSIS.				
CC	-I- SUBUNIT: INTERACTS WITH CEIAR.				
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT				
CC	FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.				
CC	-I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE				
CC	CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.				
CC	-I- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).				
CC	-I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.				

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EMBL: U24231; AAA6517.1; -

EMBL: X64709; CA559197.1; -

EMBL: BC000334; AA00034.1; -

PDB: 1A1W; 16-FEB-99.

PDB: 1A1Z; 16-FEB-99.

DR Genew; HGNC:3573; FADD.

DR MIM; 602457; -

DR InterPro; IPR001875; DED.

DR InterPro; IPR000488; Death.

DR Pfam; PF00531; death; 1.

DR Pfam; PF01335; DED; 1.

DR SMART; SM00005; DEATH; 1.

DR SMART; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS50168; DED; 1.

DR Apoptosis; 3D-structure.

FT DOMAIN 3 81 DED.

FT MUTAGEN 97 181 DEATH.

FT CONFLICT 121 121 V->N: NO INTERACTION WITH FAS RECEPTOR.

FT CONFLICT 32 32 G->V (IN REF. 2).

FT SEQUENCE 208 AA; 23279 MW; 0E65E2852E83507 CRC64;

Query Match 68.8%; Score 176; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 7.8e-164;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLVVOGSLDFFSLRLQNDLPEGHTELLRLSLRHHDLRRVDFEAGAAAGAP 140

DB 33 KRRLVVOGSLDFFSLRLQNDLPEGHTELLRLSLRHHDLRRVDFEAGAAAGAP 92

QY 141 GEEDLCAPNVICDNGKDMRRRLARQLKYSDTKIDSIEDRYPRNLTERRVRESLRINTE 200

DB 93 GEEDLCAPNVICDNGKDMRRRLARQLKYSDTKIDSIEDRYPRNLTERRVRESLRINTE 152

QY 201 KENATVAHLVGLRSCQANLVADLVQVQARLQNRSGAMSPMNSDSTSEAS 256

DB 153 KENATVAHLVGLRSCQANLVADLVQVQARLQNRSGAMSPMNSDSTSEAS 208

RESULT 2

FADD_MOUSE STANDARD; PRT; 205 AA.

ID FADD_MOUSE

AC 061160; 061082;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE FADD protein (FAS-associated death domain-containing protein)

DE (Mediator of receptor induced toxicity).

GN FADD OR MORT1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96220459; PubMed=8649383;

RA Zhang J., Winoto A.;

RT "A mouse Fas-associated protein with homology to the human MORT1/FADD

RL protein is essential for Fas-induced apoptosis."

RL Mol. Cell. Biol. 16:2756-2763(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96152659; PubMed=85565075;

RA Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;

RT "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF

RT receptor 1 signal transduction pathways".

RL Cell 84:299-308(1996).

CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR

CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE

CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX

CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8

CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC

CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE

CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.

CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).

CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL: U50406; AAB07789.1; -

EMBL: U43184; AAB97876.1; -

DR HSSP; Q13158; 1A1Z.

DR MGD; MG1:109324; Fadd.

DR InterPro; IPR001875; DED.

DR InterPro; IPR000488; Death.

DR Pfam; PF00531; death; 1.

DR Pfam; PF01335; DED; 1.

DR SMART; SM00005; DEATH; 1.

DR SMART; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS50168; DED; 1.

DR Apoptosis; 3D-structure.

FT DOMAIN 3 81 DED.

FT MUTAGEN 97 181 DEATH.

FT CONFLICT 168 168 C->F (IN REF. 2).

FT SEQUENCE 205 AA; 22960 MW; 4BC8D86B33A58783 CRC64;

Query Match 5.9%; Score 15; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 4.8e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LRRELLASLRHDL 124

DB 62 LRRELLASLRHDL 76

RESULT 3

YDHE_SCHPO STANDARD; PRT; 681 AA.

ID YDHE_SCHPO

AC 092359;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C69.14 in chromosome 1.

GN SPAC69.14.

OS Schizosaccharomyces pombe (Fission Yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowich E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellton J., Stmonds M., Squares R., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodard J., Volckert G., Aert R., Robben J., Gysompiez B.,
 RA Willems I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wandt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Siparovsky G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schistosoma mansoni pome.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: BELONGS TO THE PDM110/MP15 FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z81317; CAB03616.1;
 DR InterPro: IPR001313; Ptm110/Puf.
 DR Pfam: PF00806; Puf; 8.
 DR SMART: SM00025; Ptm110; 8.
 DR Hypothetical protein.
 SQ SEQUENCE 681 AA; 73292 MW; 755A25C68A92D727 CRC64;
 Query Match 3.5%; Score 9; DB 1; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 SVSSSLSS 66
 DB 329 SVSSSLSS 337
 RESULT 4
 ID MT21.ORYSA STANDARD; PRT; 82 AA.
 AC P94029;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein-like protein type 2.
 GN MT-2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubacteriodes; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Tainong 67; TISSUE=Root;
 RX MEDLINE=97134941; PubMed=8980501;
 RA Hsieh H.M., Liu W.K., Chang A., Huang P.C.;
 RT "RNA expression patterns of a type 2 metallothionein-like gene from
 RT rice.";
 RL Plant Mol. Biol. 32:525-529(1996).
 CC -1- FUNCTION: METALLOTHIONEIN HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
 CC -----
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 CC -----
 DR EMBL: U43530; AAC49627.1;
 DR EMBL: D89931; BAA14038.1;
 DR InterPro: IPR000347; Metallothion_15.
 DR Pfam: PF01439; Metallothio_2; 1.
 DR ProDom: PD001611; Metallothion_15; 1.
 KW Metal-binding; Metal-thiolate cluster; Multigene family.
 SQ SEQUENCE 82 AA; 7852 MW; 8DC0628B8B5E503C4 CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1; 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 131 EAGAAAGA 138
 DB 54 EAGAAAGA 61
 RESULT 5
 ID RL7.THEMA STANDARD; PRT; 128 AA.
 AC P29396;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L7/L12.
 GN RPL7 OR TM0457.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
 OC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=94232816; PubMed=8177738;
 RA Palm P., Schleper C., Arnold-Ammer I., Holz I., Meier T.,
 RA Lottspeich F., Zillig W.;
 RT "The DNA-dependent RNA-polymerase of Thermotoga maritima;
 RT characterisation of the enzyme and the DNA-sequence of the genes for
 RT the large subunits.";
 RL Nucleic Acids Res. 21:4904-4908(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=94232816; PubMed=8177738;
 RA Palm P., Schleper C., Arnold-Ammer I., Holz I., Meier T.,
 RA Lottspeich F., Zillig W.;
 RT "The DNA-dependent RNA-polymerase of Thermotoga maritima;
 RT characterisation of the enzyme and the DNA-sequence of the genes for
 RT the large subunits.";
 RL Nucleic Acids Res. 21:4904-4908(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=94232816; PubMed=8177738;
 RA Nelson K.E., Clayton R.A., Gill S.R., Glinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima.";
 RL Nature 399:323-329(1999).
 CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS
 CC INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR
 CC ACCURATE TRANSLATION.
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.

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CC
DR EMBL; Z11839; CAAT7862.1; -
DR EMBL; X72695; CAAS1245.1; -
DR EMBL; AE001723; AAD35540.1; ALT_INIT.
DR PIR; S19902; R7HG12.
DR PIR; E44466; E44466.
DR PIR; S41465; S41465.
DR HSSP; P02392; ICTF.
DR TIGR; TM0457; -
DR InterPro; IPR000206; Ribosomal_L12.
DR Pfam; PF00543; Ribosomal_L12; 1.
DR ProDom; PD001326; Ribosomal_L12; 1.
DR TrEMBL; TIGR00855; L12; 1.
DR Ribosomal protein; Complete proteome.
KW SEQUENCE 128 AA; 13457 MW; FCA849CFE85906BE CRC64;
SQ
Query Match 3.1%; Score 8; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 132 AGAAGAA 139
| | | | |
Db 45 AGAAGAA 52
RESULT 6
PER_ACEME STANDARD; PRT; 174 AA.
ID PER_ACEME STANDARD; PRT; 174 AA.
AC P12347;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Period clock protein (P230).
OS Acetabularia mediterranea (Mermald's wine glass).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Dasycladales;
OC Dasycladaceae; Acetabularia.
OX NCBI_TaxID=3138;
RN [1]
RP SEQUENCE FROM N.A.
RA Li-Weber M., de Groot E.J., Schweigler H.G.;
RT "Sequence homology of the Drosophila per locus in higher plant
RT nuclear DNA and in Acetabularia chloroplast DNA."
RL Mol. Gen. Genet. 209:1-7(1987).
CC -1- SIMILARITY: TO THE PERIOD CLOCK PROTEINS OF DROSOPHILA
CC AND MOUSE.
CC
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CC
DR EMBL; X05806; CAC34964.3; -
DR PIR; S00273; S00273.
KW Biological rhythms; Repeat; Chloroplast.
KW Domain 49 138 45 X 2 AA TANDDEM REPEATS OF G-T.
SQ SEQUENCE 174 AA; 16878 MW; E6C06770E9DDCB5D CRC64;
Query Match 3.1%; Score 8; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR HSSP; P02392; .LIFE.
DR TIGR; T04057; .
DR InterPro; IPR000206; Ribosomal_L12.
DR Pfam; PF00544; Ribosomal_L12; 1.
DR ProDom; PD001326; Ribosomal_L12; 1.
DR TrEMBL; TIGR00855; L12; 1.
DR Ribosomal protein; Complete proteome.
SQ SEQUENCE 128 AA; 13457 MW; FCA8489CFE85906BE CAC64;

	Query Match	Score 8;	DB 1;	length 128;
	Best Local Similarity	100.0%;	Pred. No. 2;	
Matches	8; Conservative	0;	Mismatches	0; Gaps 0.
OY	132 AGAAGAA	139		
Db	45 AGAAGAA	52		

RESULT 6	
PER_ACEME	
ID PER_ACEME	STANDARD;
	PRT; 174 AA.

DT 01-OCT-1989 (Rel. 12, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Period clock protein (P230).
 OS Acetabularia mediterranea (Marmaid's wine glass).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Dasycladales;
 OC Dasycladaceae; Acetabularia.
 OX NCBI_TaxID=3138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li-Weber M., de Groot E.J., Schweiger H.G.;
 RT "Sequence homology to the Drosophila per locus in higher plant
 nuclear DNA and in Acetabularia chloroplast DNA.";
 RL Mol. Gen. Genet. 209:1-7(1987).
 CC -1- SIMILARITY: TO THE PERIOD CLOCK PROTEINS OF DROSOPHILA
 AND MOUSE.

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DR
PR: 405000; CAC3904.3; .
PIR: S00273; S00273.
KW
Biological repeats: Repeat; Chloroplast.
DOMAIN 49 138
SEQUENCE 174 AA; 16878 MW; E6C06770E3DDCB5D CRC64;
SQ

Query Match	3.1%	Score 8:	DB 1:	Length 174;
Best Local	Similarity 100.0%	Pred.No. 2.7;		
Matches	8;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0

```
QY      60 SSSLSSE 67
        |||||
Db      41 SSSLSSE 48
```

RESULT /	YNW8_YEAST	STAND
ID	YNW8_YEAST	

RESULT /	STAND
YNW8_YEAST	
ID YNW8_YEAST	
AC P53862:	

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 01-OCT-1996 (Rel. 34, last annotation update)
DE Hypothetical 20.6 kDa protein in URE2-SSU72 intergenic region
DE precursor.
GN YNL228W OR N1249.
OS *Saccharomyces cerevisiae* (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;

RP SEQUENCE FROM N.A.
RX MEDLINE:97051596; PubMed-8896273;
RA Pandolfo D., de Antoni A., Lantiranchi G., Valle G.,
RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT reading frames including a novel gene encoding a globin-like
RT domain".
RL yeast 12:1071-1076(1996).
RN [2]
RP SEQUENCE OF 71-258 FROM N.A.
RA Duesterhoeft A., Floeth M., Filtz C., Heuss-Netzel D., Hilbert H.,
RA Moestl D.; (May-1996) to the EMBL/GenBank/DBJ databases.
CC Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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DR EMBL; 269381; CAA93370.1; -.
DR EMBL; 271504; CAA96131.1; -.
DR SGD: S0005172; YNL228W.

KW	Hypocretin-like protein; Signal; Transmembrane.	1	23	POTENTIAL.
FT	SIGNAL	24	258.	HYPOTHETICAL PROTEIN YML228W.
FT	CHIN	65	85	POTENTIAL.
FT	TRANSMEM	124	144	POTENTIAL.
FT	TRANSMEM	231	251	POTENTIAL.
FT	DOMAIN	79	82	POLY-PHE.
FT	DOMAIN	88	92	POLY-SER.
FT	DOMAIN	129	141	POLY-PHE.
FT	CARBOXYD	118	118	N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOXYD	206	206	N-LINKED (GLCNAC...) (POTENTIAL).
SO	SEQUENCE	258 AA;	28641 MW;	24538C70CD10E86C CRC64;

Query Match	3.1%;	Score 8;	DB 1;	length 258;
Best Local Similarity	100.0%;	Pred. No. 3.9;		
Matches	8;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
Qy	60	SSSLSSSE	67	
Db	165	SSSLSSSE	172	

RESULT	8
QCRA_MYCTU	
ID	QCRA_MYCTU
STANDARD:	
PRT:	429 AA.

ID	NAME	DATE
AC	010387;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	

ID	NAME	DATE
AC	010387;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ubiqinol-cytochrome C reductase iron-sulfur subunit (Rieske iron-
 sulfur protein).
 GN OCRA OR RV2195 OR MT2251 OR MTCY190.06.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinobacteridae;
 CC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=9825967; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Gainer T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jorgensen K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RT Nature 393:537-544(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CDC 1551 / Oshkosh;
 RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Ormazabal L.A., Esmailova M.D., Salzberg S.L.,
 RA Bacher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX. THE RIESKE PROTEIN IS A HIGH POTENTIAL 2FE-2S PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNIT OF THE UBIQUINOL-CYTOCHROME C COMPLEX.
 CC ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A CYTOCHROME C SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: TO RIESKE PROTEINS FROM OTHER SOURCES (MITOCHONDRIA,
 CC BACTERIAL, CHLOROPLAST).
 CC -----
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 CC -----
 DR EMBL: Z70283; CA94264.1;
 DR EMBL: AE007071; AA46537.1;
 DR TIGR: MT2251;
 DR Tuberculast: RV2195;
 DR InterPro: IPR001281; Rieske.
 DR Pfam: PF00355; Rieske; 1.
 DR PROSITE: PS00199; RIESKE_1; FALSE_NEG;
 DR PROSITE: PS00200; RIESKE_2; 1.
 KW Electron transport; Iron-sulfur; Oxidoreductase; Transmembrane;
 KW Complete proteome.
 FT TRANSMEM 96 116 POTENTIAL.
 FT TRANSMEM 137 157 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT METAL 353 353 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 355 355 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 372 372 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 375 375 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT DISULFID 358 374 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 46922 MW; C22C87EC283FE0EE CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 LGHYVRK 83
 Db 329 LGRVVRK 336
 RESULT 9
 ID IL9R_MOUSE STANDARD; PRT; 468 AA.
 AC 001114;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Interleukin-9 receptor precursor (IL-9R).
 GN IL9R.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=92302307; PubMed=1376929;
 RA Renauld J.C., Druet C., Kermouni A., Housiau F., Dyttenhove C.,
 RA van Roost E., Van Snick J.;
 RT "Expression cloning of the murine and human interleukin 9 receptor
 RT cDNAs."
 RT Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694(1992).
 RL -1- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-9.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M84746; AA37871.1;
 DR PIR: A45268; A45268.
 DR MGI: 96564; IL9R.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003531; Hemopoietin_S_F1.
 DR PROSITE: PS01355; HEMATOPOIETIN_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; T-cell.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 468 INTERLEUKIN-9 RECEPTOR.
 FT DOMAIN 38 270 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 271 291 POTENTIAL.
 FT DOMAIN 292 468 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 149 242 FIBRONECTIN TYPE-III.
 FT CARBOHYD 116 116 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 468 AA; 52260 MW; BBE7179FD72E29A5 CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 33 GARRAGPQ 40
 Db 328 GARRAGPQ 335
 RESULT 10
 ID NPXR_HUMAN STANDARD; PRT; 499 AA.
 AC 095502;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DR HSSP: P08837; 1GIC.
 DR InterPro: IPR001137; PTS_EI1A.
 DR InterPro: IPR001956; PTS_EI1B.
 DR InterPro: IPR003352; PTS_EI1C.
 DR Pfam: PF00358; PTS_EI1A.1.
 DR Pfam: PF00367; PTS_EI1B.1.
 DR Pfam: PF02378; PTS_EI1C.1.
 DR ProDom: PD001476; PTS_EI1B.1.
 DR ProDom: PD002483; PTS_EI1A.1.
 DR TIGRfam: TIGR00830; PTBA.1.
 DR ProSITE: PS00371; PTS_EI1A.1.
 DR ProSITE: PS01035; PTS_EI1B_CYS.1.
 DR Phosphotransferase system: Sugar transport; Transferase;
 Phosphorylation; Transmembrane
 FT DOMAIN 1 43 EI1B DOMAIN
 FT DOMAIN 1 43 EI1C DOMAIN
 FT DOMAIN 1 43 EI1A DOMAIN
 FT TRANSMEM 126 146 POTENTIAL.
 FT TRANSMEM 162 182 POTENTIAL.
 FT TRANSMEM 193 213 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 260 280 POTENTIAL.
 FT TRANSMEM 303 323 POTENTIAL.
 FT TRANSMEM 344 364 POTENTIAL.
 FT TRANSMEM 376 396 POTENTIAL.
 FT TRANSMEM 409 429 POTENTIAL.
 FT TRANSMEM 442 462 POTENTIAL.
 FT MOD_RES 28 28 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 602 602 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 683 AA; 72571 MW; 0B42CAEC60828075 CRC64.

Query Match 3.1%; Score 8; DB 1; Length 683;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 |||||
 Db 510 AGAAGAA 517

RESULT 12
 PRGR_RABIT STANDARD; PRT; 930 AA.
 AC P06186;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Progesterone receptor (PR).
 GN PGR OR NR3C3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8706449; PubMed=3538016;
 RA Loosfelt H., Atger M., Mistrall M., Guichon-Mantel A., Meriel C.,
 RA Logeat F., Benarous R., Milgrom E.;
 RT Cloning and sequence analysis of rabbit progesterone-receptor
 RT complementary DNA.
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC -1- THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC MN3 SUBFAMILY.
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DR EMBL: M4547; AAA31443.1;
 DR PIR: A25923; A25923.
 DR HSSP: P06401; 1A28.
 DR TRANSFAC: T00697;
 DR InterPro: IPR000536; Hormone_rec_119.
 DR InterPro: IPR000128; Progesterone_receptor.
 DR InterPro: IPR001628; ZnF_C4steroid.
 DR Pfam: PF00104; hormone_rec.1.
 DR Pfam: PF00105; zf-C4.1.
 DR Pfam: PF02161; Prog_receptor.1.
 DR PRINTS: PR00047; STROIDFINGER.
 DR ProDom: PD000035; ZnF_C4steroid.1.
 DR SMART: SM00430; HOL1.1.
 DR SMART: SM00399; ZnF_C4.1.
 DR ProSITE: PS00031; NUCLEAR_RECEPTOR.1.
 DR Receptor: Transcription regulation; DNA-binding; Nuclear protein;
 Zinc-finger; Steroid-binding.
 FT DOMAIN 1 565 MODULATING, PRO-RICH.
 FT DNA_BIND 568 633 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 568 588 C4-TYPE.
 FT ZN_FING 604 628 C4-TYPE.
 FT DOMAIN 678 930 STEROID-BINDING.
 FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 930 AA; 98666 MW; 644FF4C13BF883 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 930;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 GAAGAAP 140
 |||||
 Db 503 GAAGAAP 510

RESULT 13
 ID 41_DROME STANDARD; PRT; 1698 AA.
 AC Q9V8R9; Q24440; Q24441; Q24442; Q9V8R8; Q9V8S0.
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein 4.1 homolog (Coracle protein).
 GN CORA OR CG11949.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), AND FUNCTION.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=94215495; PubMed=8162854;
 RA Fejon R.G., Dawson I.A., Artavanis-Tsakonas S.;
 RT "A Drosophila homologue of membrane-skeleton protein 4.1 is associated
 RT with septate junctions and is encoded by the coracle gene."
 RL Development 120:545-557(1994).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4).
 CC STRAIN=Berkley;
 CC MEDLINE=20196006; PubMed=10731132.
 CC Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 CC Sutton G.G., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,
 CC Brandon R.C., Rogers Y.-H.C., Blasej R.G., Change M., Pfeiffer B.D.,
 CC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 CC Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 CC Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
 RA Dietrich F.S., Deltus H., DiPaolo T., Dubois E., Duesterhoeft A.,
 RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
 RA Hall J., Hobling U., Heumann K., Hilbert H., Hillier L.,
 RA Hunkeler-Smith S., Hyman R., Johnston M., Kaiman S., Klatte K.,
 RA Komp C., Kurl O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
 RA Marathe R., Messing F., Mewes H.-W., Mittipati S., Moestl D.,
 RA Mueller-Auer S., Namath A., Neutwich U., Oeffner P., Pearson D.,
 RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scherf M.,
 RA Scherens B., Schramm S., Schroeder M., Sidcu A.M., Tettein H.,
 RA Urrutazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
 RA Walsh S.V., Wandt R., Wang Y., Wedler E., Wedler H., Winnett E.,
 RA Zhong W.W., Zollner A., Vo D.H., Hani J.,
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI.",
 RL Nature 387:103-105(1997).
 RN (4)
 RP MOTAGENESIS OF GLY-1250.
 RC STRAIN-5288C;
 RX MEDLINE-94316198; PubMed-8041367;
 RA Inokoshi J., Tomoda H., Hashimoto H., Watanabe A., Takeshima H.,
 RA Omura S.;
 RT "Cerulenin-resistant mutants of *Saccharomyces cerevisiae* with an
 altered fatty acid synthase gene";
 RL Mol. Gen. Genet. 244:90-96(1994).
 CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
 LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
 CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,
 CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-
 CC CARRIER PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING
 CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH -> a
 CC long-chain fatty acid + (N+1) COA + N CO(2) + 2N NADP(+).
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
 CC carrier protein] -> 3-oxoacyl-[acyl-carrier protein] + CO(2) +
 CC [acyl-carrier protein]
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- SUBUNIT: [alpha(6)beta(6)] hexamers of two multifunctional
 CC subunits (alpha and beta).
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
 CC OTHER FUNGI.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC
 DR EMBL: J03936; AAA34601.1; -
 DR EMBL: X76890; CA54218.1; -
 DR EMBL: X94561; CA64256.1; -
 DR EMBL: Z73586; CA97947.1; -
 DR EMBL: Z73587; CA97948.1; -
 DR PIR: A31107; A31107;
 DR SGD: S0006152; FAS2;
 DR InterPro: IPR002582; ACPS;
 DR InterPro: IPR00794; ketoacyl-synt.
 DR InterPro: IPR004568; Pantethn_ttn.
 DR InterPro: IPR003880; Pantethn_attach.
 DR Pfam: PF00109; ketoacyl-synt; 1.
 DR Pfam: PF01648; ACPS; 1.
 DR Pfam: PF02801; ketoacyl-synt_C; 1.
 DR ProDom: PD004282; ACPS; 1.
 DR TIGRfams: TIGR00556; pantethn_ttn; 1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; 1.
 DR PROSITE: PS00606; B_KETOACYL-SYNTHASE; 1.
 KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
 KW Transferase; NADP; Phosphopantetheine;
 FT DOMAIN 1 ? ACTY CARRIER (ACP).
 FT 675 874 BETA-KETOACYL REDUCTASE.
 FT DOMAIN 1149 1363 BETA-KETOACYL SYNTHASE.

FT BINDING 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).
 FT ACT_SITE 1305 1305 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT MOTAGEN 1250 1250 G->S: CERULENIN-RESISTANCE.
 FT CONFLICT 310 310 G -> GTGGG (IN REF. 1).
 FT CONFLICT 594 594 T -> I (IN REF. 1).
 FT CONFLICT 941 1019 AKRKEIVETSEVRKAVSITALEHKYVNSADAYAOVE
 FT IORPANIQDPEPLKPYKQYQIAIPAEGLDLERYI ->
 FT CLNCVSMKLKLERQFSPKLSMISLMAVLMHMLMS
 FT KFNQELTFNMTSQNRNHTNRLKPLSLKVCWIMKELF
 FT (IN REF. 1).
 FT KRMEMA -> KMGNGS (IN REF. 1).
 FT A -> S (IN REF. 1).
 FT N -> T (IN REF. 1).
 FT CONFLICT 1036 1041
 FT CONFLICT 1408 1408
 FT CONFLICT 1671 1671
 SQ SEQUENCE 1887 AA; 206946 MW; 08B872734CF3AEEA CRC64;
 Query Match 3.18; Score 8; DB 1; Length 1887;
 Best Local Similarity: 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 132 AGAAGAA 139
 Db 314 AGAAGAA 321
 ID OM06_YEAST STANDARD; PRT; 61 AA.
 AC P33448;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitochondrial import receptor subunit TOM6 (Mitochondrial import-site
 DE protein ISp6) (Translocase of outer membrane 6 kDa subunit).
 DE TOM6 OR ISp6 OR YOR045W.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC *Saccharomyces*; *Saccharomycetaceae*; *Saccharomyces*.
 OX NCBI_TaxID:4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9345447; PubMed-8344244;
 RA Kassenbrock C.K., Cao W., Douglas M.G.;
 RT "Genetic and biochemical characterization of ISp6, a small
 RT mitochondrial outer membrane protein associated with the protein
 RT translocation complex";
 RL EMBO J. 12:3023-3034(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Landt O., Hiesel R., Unseld M.;
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: SEEMS TO ACT AS A MODULATOR OF THE DYNAMICS OF THE
 CC MITOCHONDRIAL PROTEIN TRANSPORT MACHINERY. SEEMS TO PROMOTE THE
 CC ASSOCIATION OF SUBUNITS OF THE OUTER MEMBRANE TRANSLOCASE.
 CC -1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT
 CC LEAST 8 DIFFERENT PROTEINS (TOM5, TOM6, TOM7, TOM20, TOM22,
 CC TOM37, TOM40 AND TOM70).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC outer membrane.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC
 DR EMBL: Z22815; CA80469.1; -
 DR EMBL: Z74953; CA99236.1; -
 DR PIR: S35320; S35320.
 DR SGD: S0005571; TOM6.
 KW Transport; Protein transport; Outer membrane; Mitochondrion;
 KW Transmembrane.

FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 32 52 POTENTIAL.
 FT DOMAIN 53 61 MITOCHONDRIAL (POTENTIAL).
 SQ SEQUENCE 61 AA; 6407 MW; EE3F295BC0FE7240 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 61;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 GAAAGAA 139
 |||||
 Db 9 GAAAGAA 15

Search completed: June 19, 2003, 10:45:50
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:44:01 ; Search time 40 Seconds
(Without alignments)
615.260 Million cell updates/sec

Title: US-09-933-814-2

Sequence: 1 VNGAPRCRGCGILGPKGR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	176	68.8	208	2	A56912	FADD protein - hum
2	9	3.5	681	2	T39076	serine rich pumili
3	8	3.1	82	2	T03727	metallothionein-11
4	8	3.1	118	2	D72524	hypothetical prote
5	8	3.1	128	1	R7HG12	ribosomal protein
6	8	3.1	174	2	S00273	period clock prote
7	8	3.1	224	2	B75460	hypothetical prote
8	8	3.1	238	2	S63194	probable membrane
9	8	3.1	291	2	A83364	proveridine biosynt
10	8	3.1	316	2	G75388	hypothetical prote
11	8	3.1	396	2	T01201	hypothetical prote
12	8	3.1	429	2	D70784	probable Rieske [2
13	8	3.1	467	2	I56896	gene gfi-2 protein
14	8	3.1	468	2	A45268	interleukin-9 rece
15	8	3.1	639	2	G86455	hypothetical prote
16	8	3.1	930	2	A25923	progesterone recep
17	8	3.1	1698	2	T13800	coracle gene prote
18	8	3.1	1887	2	S61703	fatty-acid synthas
19	8	3.1	2639	2	T31328	fibroin - Chinese
20	8	3.1	2910	2	T28156	DNA-directed RNA p
21	7	2.7	61	2	S35320	ISF6 protein - yea
22	7	2.7	73	2	H72856	Acorf-55 protein -
23	7	2.7	77	2	F70598	probable PE protei
24	7	2.7	106	2	D69808	hypothetical prote
25	7	2.7	113	2	A75626	salicylate monooxy
26	7	2.7	124	2	S45788	probable membrane
27	7	2.7	128	2	E70466	ribosomal protein
28	7	2.7	128	2	T30714	hypothetical prote
29	7	2.7	130	2	A70615	probable ribosomal

30	7	2.7	130	2	S41123	ribosomal protein
31	7	2.7	135	2	AH2100	hypothetical prote
32	7	2.7	135	2	A42098	transcription fact
33	7	2.7	141	2	T34419	hypothetical prote
34	7	2.7	150	2	A59103	hypothetical prote
35	7	2.7	158	2	F65206	probable transcript
36	7	2.7	158	2	F91243	probable transcript
37	7	2.7	158	2	D86091	serine-rich protei
38	7	2.7	163	2	T17700	hypothetical prote
39	7	2.7	183	2	S67784	probable lprb prot
40	7	2.7	185	2	B70755	proline-rich prote
41	7	2.7	188	2	D29149	regulatory factor
42	7	2.7	190	2	A83298	outer surface prot
43	7	2.7	192	2	S70267	hypothetical prote
44	7	2.7	194	2	F83219	hypothetical prote
45	7	2.7	194	2	F91169	hypothetical prote

ALIGNMENTS

RESULT 1

A56912 FADD protein - human

N:Alternate names: FAS-associating death domain containing protein FADD; mediator of

C:Species: Homo sapiens (man)

C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text-change 01-Dec-2000

C:Accession: A56912; I38041

R:Chinaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.

Cell 81, 505-512 (1995)

A:Title: FADD, a novel death domain-containing protein, interacts with the death doma

A:Reference number: A56912; MUID:95277837; PMID:7538907

A:Accession: A56912

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <CHI>

A:Cross-references: GB:U24231; NID:9809486; PIDN:AA86517.1; PID:9809487

R:Boldin, M.P.; Varfolomeev, E.E.; Pancier, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D.

J. Biol. Chem. 270, 7795-7798 (1995)

A:Title: A novel protein that interacts with the death domain of Fas/APo1 contains a

A:Reference number: I38041; MUID:95229578; PMID:7536190

A:Accession: I38041

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-31, 'V', 33-208 <RES>

A:Cross-references: EMBL:X84709; NID:9791037; PIDN:CAA59197.1; PID:9791038

A:Gene: GDB:FADD; MORT1

A:Cross-references: GDB:1320394

C:Superfamily: receptor-induced toxicity mediator MORT1

C:Keywords: apoptosis

Query Match: 68.8%; Score 176; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1,4e-162;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	81	KRKLERYQSGDLSMLEQNDLEPGHTELLRELLASLRRLDLSRRVDFEAGAAAGAP	140
DB	33	KRKLERYQSGDLSMLEQNDLEPGHTELLRELLASLRRLDLSRRVDFEAGAAAGAP	92
QY	141	GEEDLCAAFNYICNVGKDFRRRLAROLKVSPTKIDSIDRIPRNLTEVERESLAINKTE	200
DB	93	GEEDLCAAFNYICNVGKDFRRRLAROLKVSPTKIDSIDRIPRNLTEVERESLAINKTE	152
QY	201	KENATVAHLVGLALSCQNTLVADLVQEQARDLQNSGASPMNSDASTSEAS	256
DB	153	KENATVAHLVGLALSCQNTLVADLVQEQARDLQNSGASPMNSDASTSEAS	208

RESULT 2

T39076 serine rich pumilio family rna binding domain pr otein - fission yeast (Schizosacchar

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T39076
 R/Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, V.
 Submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21825
 A:Accession: T39076
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-681 <NCR>
 A:Cross-references: EMBL:281317; PIDN:CA03616.1; GSPDB:GN00066; SPDB:SPAC669.14
 A:Experimental source: strain 972h-; cosmid c669
 C/Genetics:
 A:Gene: SPDB:SPAC669.14
 A:Map position: 1
 A:Introns: 580/3

Query Match
 Best Local Similarity 100.0%; Score 9; DB 2; Length 681;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 SVSSSLSS 66
 Db 329 SVSSSLSS 337

RESULT 3
 T03727
 metallothionein-like protein - rice
 C/Species: Oryza sativa (rice)
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
 C/Accession: T03727
 R:Chen, W.M.; Hsieh, H.M.; Huang, P.C.
 Submitted to the EMBL Data Library, December 1996
 A:Description: Signification of two introns in type 2 rice metallothionein-like gene.
 A:Reference number: Z15032
 A:Accession: T03727
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <CHD>
 A:Cross-references: EMBL:DB9931; PIDN:BA14038.1
 A:Experimental source: cv. Tainung 67, root
 C/Genetics:
 A:Gene: rGMT-2
 A:Introns: 22/2; 48/2
 C:Superfamily: metallothionein

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 82;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 EAGAAAGA 138
 Db 54 EAGAAAGA 61

RESULT 4
 D72524
 hypothetical protein APE2169 - Aeropyrum pernix (strain K1)
 C/Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C/Accession: D72524
 R:Kawabeyashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahawa, H.; Takahashi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6; 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; MID:9310339; PMID:10382966
 A:Accession: D72524
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-118 <KAW>
 A:Cross-references: DDBJ:AP000063; NID:9510564; PIDN:BA81180.1; PID:41044966; PID:9510
 A:Experimental source: strain K1
 C/Genetics:

A:Gene: APE2169

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 118;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 Db 57 AGAAGAA 64

RESULT 5
 R7HG12
 ribosomal protein L7/L12 - Thermotoga maritima (strain MSB8)
 C/Species: Thermotoga maritima
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 21-Jul-2000
 C/Accession: E44466; S41465; B72376; S19902
 R:Li, D.; Dennis, P.P.
 J. Biol. Chem. 267, 22787-22797, 1992
 A:Title: The organization and expression of essential transcription translation comp
 A:Reference number: A44466; MID:93054590; PMID:1429627
 A:Accession: E44466
 A:Molecule type: DNA
 A:Residues: 1-128 <LIA>
 A:Cross-references: EMBL:Z11839; NID:9407020; PIDN:CA47862.1; PID:946187
 A>Note: sequence extracted from NCBI backbone (NCBI:118058)
 R:Palin, P.; Schleper, C.; Arnold-Himmer, I.; Holz, I.; Meyer, T.; Lottspeich, F.; Zil
 Nucleic Acids Res. 21, 4904-4908, 1993
 A:Title: The DNA-dependent RNA-polymerase of Thermotoga maritima; characterisation o
 A:Reference number: S41465; MID:94232816; PMID:8177738
 A:Accession: S41465
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 C.M.
 A:Molecule type: DNA
 A:Residues: 1-128 <PAL>
 A:Cross-references: EMBL:X72695; NID:9425255; PIDN:CA51445.1; PID:9425257
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hl
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MID:99287316; PMID:10360571
 A:Accession: B72376
 A:Molecule type: DNA
 A:Residues: 1-128 <ARN>
 A:Cross-references: GB:AE001723; GB:AE000512; NID:94980953; PIDN:AA035540.1; PID:949
 A:Experimental source: strain MS8
 C/Genetics:
 A:Gene: TM0457
 C:Superfamily: Escherichia coli ribosomal protein L12
 C:Keywords: protein biosynthesis; ribosome

Query Match
 Best Local Similarity 100.0%; Score 8; DB 1; Length 128;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 Db 45 AGAAGAA 52

RESULT 6
 S00273
 period clock protein - Acetabularia mediterranea chloroplast (fragment)
 C/Species: chloroplast Acetabularia mediterranea
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Jun-2000
 C/Accession: S00273
 R:Li-Weber, M.; de Groot, E.J.; Schweiger, H.G.
 Mol. Gen. Genet. 209, 1-7, 1987
 A:Title: Sequence homology to the Drosophila per locus in higher plant nuclear DNA a
 A:Reference number: S00273
 A:Accession: S00273
 A:Molecule type: DNA

A:Residues: 1-174 <LIV>
 A:Cross-references: EMBL:X05806; NID:g11316; PIDN:CA29249.1; PID:g1334349
 C:Genetics:
 A:Genome: chloroplast
 C:Superfamily: period clock protein; EGF homology
 C:Keywords: chloroplast; circadian rhythm
 F:49-138/Region: 2-residue repeats (G-T)

Query Match 3.1%; Score 8; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 SSSLSSE 67
 DB 41 SSSLSSE 48

RESULT 7
 B75460
 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: B75460
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 Science 266, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75460
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <WHI>
 A:Cross-references: GB:AE001944; GB:AE000513; NID:g6458634; PIDN:AA10496.1; PID:g645864
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0915
 A:Map position: 1

Query Match 3.1%; Score 8; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 173 AGAAGAA 180

RESULT 8
 S63194
 probable membrane protein YNL228w - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein N1249
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
 C:Accession: S63194; S63186; S67370; S72088
 R:Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63188
 A:Accession: S63194
 A:Molecule type: DNA
 A:Residues: 1-258 <PAV>
 A:Cross-references: EMBL:Z71504; NID:g1302248; PID:g239626; PID:g1302249; MIPS:YNL228w
 A:Experimental source: strain S788C
 R:Duesterheft, A.; Floeth, M.; Fritze, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62944
 A:Accession: S63186
 A:Molecule type: DNA
 A:Residues: 71-258 <DUE>
 A:Cross-references: EMBL:Z71504; MIPS:YNL228w
 A:Experimental source: strain S288C
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the EMBL Data Library, February 1996

A:Description: DNA sequence of cosmid 14-5 from chromosome XIV.
 A:Reference number: S67355
 A:Accession: S67370
 A:Molecule type: DNA
 A:Residues: 1-258 <PAV>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PID:e221816; PID:g1183986
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 Yeast 12, 1071-1076, 1996
 A:Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading
 A:Reference number: S72073; MUID:97051596; PMID:8896273
 A:Accession: S72088
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-258 <PAV>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CA93370.1; PID:g1183986
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Genetics:
 A:Cross-references: SGD:S0005172
 A:Map position: 14L
 A:Note: YNL228w
 C:Keywords: transmembrane protein
 F:723/Domain: transmembrane #status predicted <TM1>
 F:65-81/Domain: transmembrane #status predicted <TM2>
 F:129-145/Domain: transmembrane #status predicted <TM3>
 F:230-246/Domain: transmembrane #status predicted <TM4>

Query Match 3.1%; Score 8; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 SSSLSSE 67
 DB 165 SSSLSSE 172

RESULT 9
 A83364
 pyoverdine biosynthesis protein PycB PA2255 [Imported] - *Pseudomonas aeruginosa* (stra
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: A83364
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: A83364
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-291 <STO>
 A:Cross-references: GB:AE004651; GB:AE004091; NID:g9948277; PIDN:AA05643.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: pycB; PA2255

Query Match 3.1%; Score 8; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRR 120
 DB 224 ELASLRR 231

RESULT 10
 G75388
 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: G75388
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; PMID:10567266

A:Accession: G75388

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1316 <NH2>

A:Cross-references: GB:AE001993; GB:AE000513; NID:96459244; PIDN:AAE11061.1; PID:9645925

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1483

A:Map position: 1

Query Match 3.1%; Score 8; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
DB 138 AGAAGAA 145

RESULT 11

T01201

hypothetical protein F21E10.13 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999

C/Accession: T01201

R:Davidson, S.; Rohlfing, T.; David, M.; O'Brian, D.

submitted to the EMBL Data Library, April 1998

A:Description: The sequence of A. thaliana F21E10.

A:Reference number: Z14258

A:Accession: T01201

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-396 <NAV>

A:Cross-references: EMBL:AF058914; NID:93047074; PID:93047085; GSPDB:GN00063; ATSP:F21E10

C:Genetics:

A:Gene: ATSP:F21E10.13

A:Map position: 5

A:Introns: 54/1; 101/2; 196/3; 274/3

Query Match 3.1%; Score 8; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 15;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 SVSSSLSS 65
DB 328 SVSSSLSS 335

RESULT 12

D70784

probable Rheske [2Fe-2S] iron-sulfur protein cyob - *Mycobacterium tuberculosis* (strain H37Rv)

C:Species: *Mycobacterium tuberculosis*

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C/Accession: D70784

R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: D70784

A:Status: preliminary

A:Molecule type: nucleic acid sequence not shown; translation not shown

A:Residues: 1-429 <COL>

A:Cross-references: GB:270283; GB:AL123456; NID:93261561; PIDN:CAA94264.1; PID:6233571.

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: qcrA

Query Match 3.1%; Score 8; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 GARRAGPO 40
DB 328 GARRAGPO 335

C:Superfamily: Rheske [2Fe-2S] homology
C:Keywords: 2Fe-2S; metalloprotein; Rheske iron-sulfur protein
F:33-389/Domin: Rheske [2Fe-2S] homology <RS>
F:333,355,372,375/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #stat

Query Match 3.1%; Score 8; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 LGRVYKRK 83
DB 329 LGRVYKRK 336

RESULT 13

I56896

gene gfi-2: protein - rat

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C/Accession: I56896

R:Pinbacher, M.M.; Bear, S.E.; Tschlis, P.N.

J. Virol. 68, 7709-7716, 1994

A:Title: Replacement of interleukin-2 (IL-2)-generated mitogenic signals by a mink c

ed leukemogenesis.

A:Reference number: I56896; PMID:95055995; PMID:7866560

A:Accession: I56896

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <RS>

A:Cross-references: GB:IJ6459; NID:9598371; PIDN:AAA63702.1; PID:9598372

C:Genetics:

A:Gene: gfi-2

Query Match 3.1%; Score 8; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 GARRAGPO 40
DB 327 GARRAGPO 334

RESULT 14

A45268

interleukin-9 receptor precursor - mouse

C:Species: *Mus musculus* (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999

C/Accession: A45268

R:Renaldi, J.C.; Druet, C.; Kermouni, A.; Housiau, F.; Dyttenhove, C.; Van Roost, E.

Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992

A:Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.

A:Reference number: A45268; PMID:92302307; PMID:1376929

A:Accession: A45268

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-468 <REN>

A:Cross-references: GB:N84746; NID:9194044; PIDN:AAA37871.1; PID:9194045

A:Note: authors translated the codon GGG for residue 394 as Glu

C:Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 3.1%; Score 8; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 GARRAGPO 40
DB 328 GARRAGPO 335

RESULT 15

G86455

hypothetical protein T1609.7 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:/Accession: G86455
R:/Phenology: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:/Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:/Reference number: A86141; MUID:21016719; PMID:1130712
A:/Accession: G86455
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-639 <STO>
A:/Cross-references: GB:AE005172; NID:g11054708; PIDN:AA627902.1; GSPDB:GN00141
C:/Genetics:
A:/Map position: 1

Query Match 3.1%; Score 8; DB 2; Length 639;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 SSSLSSE 67
| | | | | | | | | |
DB 79 SSSLSSE 86

Search completed: June 19, 2003, 10:47:16
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:46:36 ; Search time: 21 Seconds

(without alignments)
1319.093 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VNQAPECRFGGIGLPLGKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: Gapped: 60.0, Gapext: 60.0

Searched: 417779 seqs, 108206813 residues

Word size: 0

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCN_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	256	10 US-09-933-814-2	Sequence 2, Appl1
2	256	100.0	256	10 US-09-824-134-2	Sequence 25, Appl1
3	74	28.9	74	9 US-10-112-793-25	Sequence 5, Appl1
4	74	28.9	74	9 US-10-287-354-5	Sequence 5, Appl1
5	52	20.3	82	10 US-09-952-768-64	Sequence 64, Appl1
6	51	19.9	84	10 US-10-001-254-39	Sequence 39, Appl1
7	49	19.1	81	10 US-09-410-194-9	Sequence 9, Appl1
8	45	17.6	77	9 US-10-001-254-35	Sequence 35, Appl1
9	45	17.6	77	9 US-10-013-379-7	Sequence 7, Appl1
10	3.1	3.1	128	9 US-10-013-379-7	Sequence 8, Appl1
11	3.1	3.1	128	9 US-10-013-379-8	Sequence 8, Appl1
12	3.1	3.1	311	12 US-10-062-254-288	Sequence 288, App
13	3.1	3.1	464	9 US-09-764-891-3991	Sequence 3991, Ap
14	3.1	3.1	468	10 US-09-965-313-8	Sequence 8, Appl1
15	3.1	3.1	502	10 US-09-791-378-672	Sequence 672, App
16	3.1	3.1	537	9 US-10-184-644-459	Sequence 459, App
17	3.1	3.1	537	9 US-10-184-634-459	Sequence 459, App
18	3.1	3.1	610	9 US-10-123-155-493	Sequence 493, App
19	3.1	3.1	683	9 US-09-738-626-6961	Sequence 6961, App

20	8	3.1	902	9	US-10-184-644-303	Sequence 303, App
21	8	3.1	902	9	US-10-184-634-303	Sequence 303, App
22	8	3.1	997	9	US-10-184-644-23	Sequence 23, Appl1
23	8	3.1	997	9	US-10-184-634-23	Sequence 23, Appl1
24	8	3.1	1027	9	US-10-184-644-127	Sequence 127, App
25	8	3.1	1027	9	US-10-184-634-127	Sequence 127, App
26	8	3.1	1106	9	US-10-184-644-535	Sequence 535, App
27	8	3.1	1106	9	US-10-184-634-535	Sequence 535, App
28	8	3.1	1121	9	US-10-123-155-23	Sequence 23, Appl1
29	8	3.1	1158	9	US-10-184-644-437	Sequence 437, App
30	8	3.1	1158	9	US-10-184-644-437	Sequence 437, App
31	8	3.1	1220	9	US-10-184-644-557	Sequence 557, App
32	8	3.1	1220	9	US-10-184-644-557	Sequence 557, App
33	8	3.1	1305	9	US-10-123-155-803	Sequence 303, App
34	8	3.1	1346	9	US-10-123-155-481	Sequence 481, App
35	8	3.1	1376	9	US-10-123-155-161	Sequence 161, App
36	8	3.1	1449	9	US-10-184-644-375	Sequence 375, App
37	8	3.1	1449	9	US-10-184-644-375	Sequence 375, App
38	8	3.1	1496	9	US-10-123-155-287	Sequence 287, App
39	8	3.1	1514	9	US-10-123-155-329	Sequence 329, App
40	8	3.1	1523	9	US-10-123-155-429	Sequence 429, App
41	8	3.1	1547	9	US-10-123-155-11	Sequence 11, Appl1
42	8	3.1	1579	9	US-10-184-644-441	Sequence 441, App
43	8	3.1	1579	9	US-10-184-634-441	Sequence 441, App
44	8	3.1	1671	9	US-10-184-644-505	Sequence 505, App
45	8	3.1	1671	9	US-10-184-634-505	Sequence 505, App

ALIGNMENTS

```
RESULT 1
US-09-933-814-2
Sequence 2, Application US/09933814
Patent No. US20020058798A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VAREFOLOMEY, Eugene
APPLICANT: MERT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL RECEPTORS
FILE REFERENCE: WALLACH-16B
CURRENT APPLICATION NUMBER: US/09/933,814
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/860,082
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: PCT/US95/16542
PRIOR FILING DATE: 1995-12-14
PRIOR APPLICATION NUMBER: IL 112022
PRIOR FILING DATE: 1994-12-15
PRIOR APPLICATION NUMBER: IL 112692
PRIOR FILING DATE: 1995-02-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-09-933-814-2
Query Match
Best Local Similarity 100.0%; Score 256; DB 10; Length 256;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VNQAPECRFGGIGLPLGKRDLARASPPREGARRAGOPRPLADPMPDFVLLSHVS 60
1 VNQAPECRFGGIGLPLGKRDLARASPPREGARRAGOPRPLADPMPDFVLLSHVS 60
1 VNQAPECRFGGIGLPLGKRDLARASPPREGARRAGOPRPLADPMPDFVLLSHVS 60
61 SSLSSELTETKFCICGRVYRKLERVOSGIDLSMLEQNDLPGFTELLRELLASLR 120
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61 SSLSSELTETKFCICGRVYRKLERVOSGIDLSMLEQNDLPGFTELLRELLASLR 120
121 HDLRRYDDPFGAAGAAAPBEDLCAFNVICNVGDMRRLARQLKVSOTKIDSIEDR 180
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Db 121 HDLRRVDDPEAAGAAAGAEEDLCAAFNVICDNGKDWRRRLAROLKYSDFITDSIEDR 180
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Db 181 YPRNLTERVESLRINKNTEKENATVAHLVGLRSCOMNLVADLYOEVOQARDLQNRSGA 240
QY 241 MSPMSNNSDASTSEAS 256
Db 241 MSPMSNNSDASTSEAS 256

RESULT 2
US-09-824-134-2
Sequence 2, Application US/09824134
Patent No. US20020082401A1

GENERAL INFORMATION:
APPLICANT: WALLACH, David

BOLDIN, Mark
VARPOLOMEY, Eugene
METT, Igor

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,134
FILING DATE: 03-Apr-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/860,082
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-1995
APPLICATION NUMBER: IL 114615
FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-16
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: Linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-824-134-2

Query Match 100.0%; Score 256; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 1,1e-225;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VNAPPCRFGGGIGIPGKRDRLARASEPRREGARRRAGPOPRPLADADMOPEVLILSYVS 60
QY 61 SLSSESELTELKFLCGRVYKRLERVOSGLDFSMLEONDLPEGHTELLRELLASLR 120

Db 61 SLSSESELTELKFLCGRVYKRLERVOSGLDFSMLEONDLPEGHTELLRELLASLR 120
QY 121 HDLRRVDDPEAAGAAAGAEEDLCAAFNVICDNGKDWRRRLAROLKYSDFITDSIEDR 180
Db 121 HDLRRVDDPEAAGAAAGAEEDLCAAFNVICDNGKDWRRRLAROLKYSDFITDSIEDR 180
QY 181 YPRNLTERVESLRINKNTEKENATVAHLVGLRSCOMNLVADLYOEVOQARDLQNRSGA 240
Db 181 YPRNLTERVESLRINKNTEKENATVAHLVGLRSCOMNLVADLYOEVOQARDLQNRSGA 240
QY 241 MSPMSNNSDASTSEAS 256
Db 241 MSPMSNNSDASTSEAS 256

RESULT 3
US-10-112-793-25
Sequence 25, Application US/10112793
Publication No. US20020192729A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-112-793-25

Query Match 28.9%; Score 74; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.4e-60;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDVVGQDMWRRLARQLVSDTKIDSIEDRYPNLTERTVRSRLRWKTEKENATVAHLVVG 211
Db 1 ICDVVGQDMWRRLARQLVSDTKIDSIEDRYPNLTERTVRSRLRWKTEKENATVAHLVVG 211
QY 212 ALRSCOMNLVADLV 225
Db 212 ALRSCOMNLVADLV 225
QY 61 ALRSCOMNLVADLV 74

RESULT 4
US-10-287-594-5
Sequence 5, Application US/10287594
Publication No. US20030096288A1
GENERAL INFORMATION:
APPLICANT: N1, Jian
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: RAIDD, A No. US20030096288A1a1 Deact adaptor Molecule
FILE REFERENCE: 1488.0860002
CURRENT APPLICATION NUMBER: US/10/287,594
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US/09/545,605
PRIOR FILING DATE: 2001-04-07
PRIOR APPLICATION NUMBER: 08/995,159
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60,033,868
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-594-5

Query Match
Best Local Similarity 100.0%; Score 74; DB 9; Length 74;
Pred. No. 4,4e-60; Mismatches 0; Indels 0; Gaps 0;
Matches 74; Conservative 0;

QY 152 ICDVNGKDMRLARLAKVSPDKIDSIEDRYPRNLTERRVRESLRIRKNTKRNATVAHLVG 211
DB 1 ICDVNGKDMRLARLAKVSPDKIDSIEDRYPRNLTERRVRESLRIRKNTKRNATVAHLVG 60

QY 212 ALRSCOMLVADLV 225
DB 61 ALRSCOMLVADLV 74

RESULT 5
US-10-035-408-5
Sequence 5, Application US/10035408
Patent No. US20020123117A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark P.
VARFOLOMEYEV, Eugene E.
PANCER, Zeev
METT, Igor
GONCHAROV, Tanya M.
WEINMURZEL, Henry
TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROADY AND NETMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/035,408
FILING DATE: 04-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
APPLICATION NUMBER: IL 112,742

FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROADY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-035-408-5

Query Match
Best Local Similarity 100.0%; Score 62; DB 12; Length 62;
Pred. No. 3,4e-49; Mismatches 0; Indels 0; Gaps 0;
Matches 62; Conservative 0;

QY 160 WRRLARLKVSGDTKIDEDRPRLTERRVRESLRIRKNTKRNATVAHLVGALRSCOMN 219
DB 1 WRRLARLKVSGDTKIDEDRPRLTERRVRESLRIRKNTKRNATVAHLVGALRSCOMN 60

QY 220 LV 221
DB 61 LV 62

RESULT 6
US-09-952-768-64
Sequence 64, Application US/09952768
Patent No. US20020035242A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note="human FADD"
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-952-768-64

Query Match          20.3%: Score 52; DB 10; Length 84;
Best Local Similarity 100.0%: Pred. No. 6e-40;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRRVDFEA 132
DB 33 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRRVDFEA 84

RESULT 7
US-10-001-254-39
; Sequence 39, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Stenner-Illwein, Frank
; TITLE OF INVENTION: NO. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-39

Query Match          19.9%: Score 51; DB 9; Length 82;
Best Local Similarity 100.0%: Pred. No. 4.8e-39;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRRVDFE 131
DB 31 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRRVDFE 81

RESULT 8
US-09-410-194-9
; Sequence 9, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Immler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schreier, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steinert, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
```

```

; APPLICANT: French, E. Iais
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-9

Query Match          19.1%: Score 49; DB 10; Length 81;
Best Local Similarity 100.0%: Pred. No. 3.2e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRRVDD 129
DB 33 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRRVDD 81

RESULT 9
US-10-001-254-35
; Sequence 35, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Stenner-Illwein, Frank
; TITLE OF INVENTION: NO. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-35

Query Match          17.6%: Score 45; DB 9; Length 77;
Best Local Similarity 100.0%: Pred. No. 1.4e-33;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRR 125
DB 33 KRRLERVOSGIDLFMSMLEQNDLEPGHTELLRELLASLRHRDILRR 77

RESULT 10
US-10-013-379-7
; Sequence 7, Application US/10013379
; Publication No. US20020188108A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Cate, Jamie H.
; APPLICANT: No. US20020188108A1e1, Harry F.
; APPLICANT: Yusupova, Mariat M.
; APPLICANT: Yusupova, Guinara ZH
```

APPLICANT: Baucum, Albion
APPLICANT: Lancaster, Laura
TITLE OF INVENTION: X-RAY CRYSTAL STRUCTURES OF FUNCTIONAL
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL MESSENGER RNAs
FILE REFERENCE: 19629-7010
CURRENT APPLICATION NUMBER: US/10/013,379
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US 60/254,603
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: US 60/278,013
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/294,394
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 128
TYPE: PRT
ORGANISM: Thermotoga maritima
FEATURE:
OTHER INFORMATION: 50S ribosomal protein L7
OTHER INFORMATION: 191Y1
US-10-013-379-7

Query Match
Best Local Similarity 100.0%; Score 8; DB 9; Length 128;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
DB 45 AGAAGAA 52

RESULT 11
US-10-013-379-8
Sequence 8, Application US/10013379
Publication No. US20020188108A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Cate, Jamie H.
APPLICANT: NO. US20020188108A1, Harry F.
APPLICANT: Yusupov, Marat M.
APPLICANT: Yusupov, Gulnara ZH
APPLICANT: Baucum, Albion
APPLICANT: Lancaster, Laura
APPLICANT: Dallas, Anne
TITLE OF INVENTION: X-RAY CRYSTAL STRUCTURES OF FUNCTIONAL
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL MESSENGER RNAs
FILE REFERENCE: 19629-7010
CURRENT APPLICATION NUMBER: US/10/013,379
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US 60/254,603
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: US 60/278,013
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/294,394
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 128
TYPE: PRT
ORGANISM: Thermotoga maritima
FEATURE:
OTHER INFORMATION: 50S ribosomal protein L12
OTHER INFORMATION: 191Y3
US-10-013-379-8

Query Match
Best Local Similarity 100.0%; Score 8; DB 9; Length 128;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
DB 45 AGAAGAA 52

RESULT 12
US-10-062-254-288
Sequence 288, Application US/10062254
Patent No. US20020138882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yixen
APPLICANT: Hanke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Niu, Xiping
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/156899
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/157287
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/169767
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171054
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/172958
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/171515
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 288
LENGTH: 311
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-062-254-288

Query Match
Best Local Similarity 100.0%; Score 8; DB 12; Length 311;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
DB 252 AGAAGAA 259

RESULT 13
US-09-764-891-3991
Sequence 3991, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3991
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (310)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (397)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (399)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3991

Query Match 3.18; Score 8; DB 9; Length 464;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 AGAAGAA 139
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DB 284 AGAAGAA 291

RESULT 14
US-09-965-313-8
Sequence 8; Application US/09965313
Patent No. US2002090680A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: NO. US2002090680A1 IL-9/IL-2 Receptor-Like Molecules
FILE REFERENCE: 5800-17A
CURRENT APPLICATION NUMBER: US/09/965,313
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/313,913
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 468
TYPE: PRT
ORGANISM: Mus musculus
US-09-965-313-8

Query Match 3.18; Score 8; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GARRAGPQ 40
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DB 328 GARRAGPQ 335

RESULT 15
US-09-791-378-672
Sequence 672; Application US/09791378
Patent No. US20020142303A1
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 9195-061-999
CURRENT APPLICATION NUMBER: US/09/791,378

CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 672
LENGTH: 502
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-378-672

Query Match 3.18; Score 8; DB 10; Length 502;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 AAGAAPE 142
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DB 115 AAGAAPE 122

Search completed: June 19, 2003, 10:54:23
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 19, 2003, 10:45:36 ; Search time 26 Seconds
(Without alignments)
289,703 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VNAPECRFGGILGPIGKR.....RSGAMSPMWSNDASTSEAS 256

Scoring table: OLIGO
Gapop: 60.0, Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued: Patents.AA.*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	256	4	US-08-983-502-2
2	256	100.0	256	5	PCT-US95-16542-2
3	256	100.0	256	5	PCT-US96-10521-2
4	208	81.2	208	1	US-08-618-164-3
5	176	68.8	208	4	US-09-074-044A-19
6	114	44.5	201	4	US-09-064-414-2
7	114	44.5	208	4	US-09-064-414-6
8	108	42.2	201	4	US-09-064-414-4
9	100	39.1	208	4	US-09-382-155-19
10	85	33.2	85	4	US-09-042-785A-28
11	74	28.9	74	4	US-08-995-159-5
12	74	28.9	74	4	US-08-828-683A-25
13	62	24.2	62	4	US-08-894-626-5
14	52	20.3	84	1	US-08-665-230-64
15	52	20.3	84	4	US-09-291-692-64
16	51	19.9	83	4	US-09-382-155-15
17	51	19.9	83	4	US-09-074-044A-15
18	8	3.1	379	1	US-08-164-614A-8
19	8	3.1	379	2	US-08-456-489B-8
20	8	3.1	468	2	US-08-164-614A-7
21	8	3.1	468	2	US-08-456-489B-7
22	7	2.7	22	3	US-08-940-095-40
23	7	2.7	22	3	US-08-940-093-40
24	7	2.7	22	3	US-08-940-096-40
25	7	2.7	22	4	US-09-465-719-40
26	7	2.7	22	4	US-09-453-605-40
27	7	2.7	22	4	US-09-453-838-40

28	7	2.7	47	1	US-08-209-747-24	Sequence 24, Appl
29	7	2.7	47	1	US-08-209-747-26	Sequence 26, Appl
30	7	2.7	47	1	US-08-458-298-24	Sequence 24, Appl
31	7	2.7	47	1	US-08-458-298-26	Sequence 26, Appl
32	7	2.7	48	1	US-08-209-747-21	Sequence 21, Appl
33	7	2.7	48	1	US-08-458-298-21	Sequence 21, Appl
34	7	2.7	49	1	US-08-209-747-32	Sequence 22, Appl
35	7	2.7	49	1	US-08-458-298-32	Sequence 22, Appl
36	7	2.7	50	1	US-08-209-747-27	Sequence 27, Appl
37	7	2.7	50	1	US-08-458-298-27	Sequence 27, Appl
38	7	2.7	51	1	US-08-209-747-30	Sequence 30, Appl
39	7	2.7	51	1	US-08-209-747-30	Sequence 30, Appl
40	7	2.7	51	1	US-08-458-298-30	Sequence 30, Appl
41	7	2.7	51	1	US-08-458-298-30	Sequence 30, Appl
42	7	2.7	54	1	US-08-209-747-29	Sequence 29, Appl
43	7	2.7	54	1	US-08-458-298-29	Sequence 29, Appl
44	7	2.7	55	1	US-08-209-747-10	Sequence 10, Appl
45	7	2.7	55	1	US-08-209-747-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-983-502-2
Sequence 2, Application US/08983502
Patent No. 639327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Taty V. GOLITSEY
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-2

Query Match 100.0%; Score 256; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRFGGILGFLGRRLDARASEPTEGARRAGOPRPLADPADPFLVLLHSVS 60
DB 1 VNOAPECRFGGILGFLGRRLDARASEPTEGARRAGOPRPLADPADPFLVLLHSVS 60
QY 61 SLSLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRELLASLR 120
DB 61 SLSLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRELLASLR 120
QY 121 HDLLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRLAROLKYSDFKIDSIEDR 180
DB 121 HDLLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRLAROLKYSDFKIDSIEDR 180
QY 181 YPRNLTERVRESIRIKNTEKENATVAHLVGAIRSCOMLVADLVEVOQARDLQNRSGA 240
DB 181 YPRNLTERVRESIRIKNTEKENATVAHLVGAIRSCOMLVADLVEVOQARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 2

PCT-US95-16542-2
Sequence 2, Application PC/TUS9516542

GENERAL INFORMATION:
APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
APPLICANT: WEINMORZEL, Henry
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VARELOMEY, Eugene
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
STATE: D.C.
CITY: Washington
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16542
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114615
FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
TELEX: 248633
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16542-2

Query Match 100.0%; Score 256; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRFGGILGFLGRRLDARASEPTEGARRAGOPRPLADPADPFLVLLHSVS 60
DB 1 VNOAPECRFGGILGFLGRRLDARASEPTEGARRAGOPRPLADPADPFLVLLHSVS 60
QY 61 SLSLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRELLASLR 120
DB 61 SLSLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRELLASLR 120
QY 121 HDLLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRLAROLKYSDFKIDSIEDR 180
DB 121 HDLLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRLAROLKYSDFKIDSIEDR 180
QY 181 YPRNLTERVRESIRIKNTEKENATVAHLVGAIRSCOMLVADLVEVOQARDLQNRSGA 240
DB 181 YPRNLTERVRESIRIKNTEKENATVAHLVGAIRSCOMLVADLVEVOQARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 3

PCT-US96-10521-2
Sequence 2, Application PC/TUS9610521

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-us96-10521-2

Query Match 100.0%; Score 256; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNAPBECRFGGIGLPGIKRDLARASEPTEGARBRAPQPRPLADAMPFLVLLSYVS 60
DB 1 VNAPBECRFGGIGLPGIKRDLARASEPTEGARBRAPQPRPLADAMPFLVLLSYVS 60
QY 61 SLSSELTETKFLCIGRVYRKLERVQSGIDLFSLLEQNDLEPGHTELLRELLASLR 120
DB 61 SLSSELTETKFLCIGRVYRKLERVQSGIDLFSLLEQNDLEPGHTELLRELLASLR 120
QY 121 HDLLRRVDDEAGAAAGAEEDLCAAFNYICDNGKDWRRRLARQLKVSPTKIDSTEDR 180
DB 121 HDLLRRVDDEAGAAAGAEEDLCAAFNYICDNGKDWRRRLARQLKVSPTKIDSTEDR 180
QY 181 YPRULTEVRRESLRITKTEKENATVAHLVGLRSCOMNLVADLVQEVQARDLQNRSGA 240
DB 181 YPRULTEVRRESLRITKTEKENATVAHLVGLRSCOMNLVADLVQEVQARDLQNRSGA 240
QY 241 MSPSMNSDASTSEAS 256
DB 241 MSPSMNSDASTSEAS 256

RESULT 4
US-08-618-164-3
Sequence 3, Application US/08618164
Patent No. 5712115

GENERAL INFORMATION:

APPLICANT: Hawking, Phillip R.
APPLICANT: Braxton, Scott Michael
TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,164
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0058 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-0195
TELEFAX: 415-852-0555

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 791038
US-08-618-164-3

Query Match 81.2%; Score 208; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.9e-188;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSLSSELTETKFLCIGRVYRKLERVQSGIDLFSLLEQNDLEPGH 108
DB 1 MDPLVLLHSVSSLSSELTETKFLCIGRVYRKLERVQSGIDLFSLLEQNDLEPGH 108
QY 109 ELLELLASLRHDLRRVDDEAGAAAGAEEDLCAAFNYICDNGKDWRRRLARQLK 168
DB 61 ELLELLASLRHDLRRVDDEAGAAAGAEEDLCAAFNYICDNGKDWRRRLARQLK 120
QY 169 VSDTKIDSTEDRYRNLTERVRESLRITKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
DB 121 VSDTKIDSTEDRYRNLTERVRESLRITKTEKENATVAHLVGLRSCOMNLVADLVQEV 180
QY 229 QOARDLQNRSGAMPMSWNSDASTSEAS 256
DB 181 QOARDLQNRSGAMPMSWNSDASTSEAS 208

RESULT 5

US-09-074-044A-19
Sequence 19, Application US/09074044A
Patent No. 6207458

GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NR-XB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-19

Query Match 68.8%; Score 176; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.3e-158;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRKIERVOSGLDLSMILEONDEPGHTELLRELLASLRHDLRRVDFEAGAAAGAP 140
DB 33 KRKIERVOSGLDLSMILEONDEPGHTELLRELLASLRHDLRRVDFEAGAAAGAP 92
OY 141 GEEDICAFNVICDNGKDMRRLAROLKVSPTKIDSTEDRPRLTERVRESLTKWTE 200
DB 93 GEEDICAFNVICDNGKDMRRLAROLKVSPTKIDSTEDRPRLTERVRESLTKWTE 152
OY 201 KENATVAHVGLALSCOMNLVADLVQEVQARLDQNSGAMSPMSWSDASTSEAS 256
DB 153 KENATVAHVGLALSCOMNLVADLVQEVQARLDQNSGAMSPMSWSDASTSEAS 208

RESULT 6
US-09-064-414-2
Sequence 2, Application US/09064414
Patent No. 6248875

GENERAL INFORMATION:

APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-4117
TELEFAX: (973) 683-4117

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-2

Query Match 44.5%; Score 114; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELIASLRHDLRRVDFEAGAAAGAPGEEDICAFNVICDNGKDMRRLAROLKYSDT 172
DB 58 ELIASLRHDLRRVDFEAGAAAGAPGEEDICAFNVICDNGKDMRRLAROLKYSDT 117
OY 173 KIDSIEDRPRLTERVRESLTKWTEKENATVAHVGLALSCOMNLVADLVQ 226
DB 118 KIDSIEDRPRLTERVRESLTKWTEKENATVAHVGLALSCOMNLVADLVQ 171

RESULT 7

US-09-064-414-6
Sequence 6, Application US/09064414
Patent No. 6248875

GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-6

Query Match 44.5%; Score 114; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 HTELLRELLASLRHDLRRVDFEAGAAAGAPGEEDICAFNVICDNGKDMRRLARQ 166
DB 59 HTELLRELLASLRHDLRRVDFEAGAAAGAPGEEDICAFNVICDNGKDMRRLARQ 118
OY 167 LKVSPTKIDSTEDRPRLTERVRESLTKWTEKENATVAHVGLALSCOMNL 220
DB 119 LKVSPTKIDSTEDRPRLTERVRESLTKWTEKENATVAHVGLALSCOMNL 172

RESULT 8

US-09-064-414-4
Sequence 4, Application US/09064414
Patent No. 6248875

GENERAL INFORMATION:

APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-4

Query Match 42.2%; Score 108; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 66-94;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 ELIASRRDLRRVDFEAGAAAGPEEDICAAFNVCIDNVGKDWRLARQLKVSDF 172
DB 58 ELIASRRDLRRVDFEAGAAAGPEEDICAAFNVCIDNVGKDWRLARQLKVSDF 117
QY 173 KIDSIEERYRNLTERRVRESLRIMKNTKRNATVAHVGLRSCOML 220
DB 118 KIDSIEERYRNLTERRVRESLRIMKNTKRNATVAHVGLRSCOML 165

RESULT 9
US-09-382-155-19
Sequence 19, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATENTIN AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-19

Query Match 39.1%; Score 100; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.1e-86;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKDWRLARQLKVSDFKIDSIEDRYPNLTERRVRESLRIMKNTKRNATVAHVGLRSC 216
DB 109 GKDWRLARQLKVSDFKIDSIEDRYPNLTERRVRESLRIMKNTKRNATVAHVGLRSC 168
QY 217 QANLYADLYQEQARQLQNRSGAMSPKSNDSASTSEAS 256
DB 169 QANLYADLYQEQARQLQNRSGAMSPKSNDSASTSEAS 208

RESULT 10
US-09-042-785A-28

Sequence 28, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHAYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-09-042-785A-28

Query Match 33.2%; Score 85; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.2e-72;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LCAAFNYICDVGKDWRLARQLKVSDFKIDSIEDRYPNLTERRVRESLRIMKNTKRNATVAHVGLRSCOML 204
DB 1 LCAAFNYICDVGKDWRLARQLKVSDFKIDSIEDRYPNLTERRVRESLRIMKNTKRNATVAHVGLRSCOML 60
QY 205 TVAHVGLRSCOMLTVADLYQEQV 229
DB 61 TVAHVGLRSCOMLTVADLYQEQV 85

RESULT 11
US-08-995-159-5
Sequence 5, Application US/08995159
Patent No. 6130079
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/995,159
APPLICATION NUMBER: US/08/995,159
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,868
FILING DATE: 20-DEC-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488, 0860001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2500
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-995-159-5

Query Match 28.9%; Score 74; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-62;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGDMRLANQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENAVVAHLVG 211
DB 1 ICDNVGDMRLANQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENAVVAHLVG 60
QY 212 ALRSCQMLVADLV 225
DB 61 ALRSCQMLVADLV 74

RESULT 12
US-08-828-683A-25
Sequence 25, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-828-683A-25

Query Match 28.9%; Score 74; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-62;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGDMRLANQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENAVVAHLVG 211
DB 1 ICDNVGDMRLANQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENAVVAHLVG 60
QY 212 ALRSCQMLVADLV 225
DB 61 ALRSCQMLVADLV 74

RESULT 13
US-08-894-626-5
Sequence 5, Application US/08894626
Patent No. 635780
GENERAL INFORMATION:

APPLICANT: WALLACH, David

BOLDIN, Mark P.
VARPOLOMEY, Eugene E.
PANCER, Zeev

WETT, Igor
GONCHAROV, Tanya M.

WEINMURZEL, Henry

TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington

STATE: D.C.

COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995

APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995

APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 62 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-08-694-626-5

Query Match 24.2%; Score 62; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9e-51;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 WRRLAROLKVSDFRISIEDRYPRNLTERVRESLRIRKNTKEKNAVVAHLVGLRSCOM 219
DB 1 WRRLAROLKVSDFRISIEDRYPRNLTERVRESLRIRKNTKEKNAVVAHLVGLRSCOM 60

QY 220 LV 221
DB 61 LV 62

RESULT 14
US-08-665-220-64
Sequence 64, Application US/08665220
Patent No. 5786173

GENERAL INFORMATION:

APPLICANT: Alnemir, Emaad S.
APPLICANT: Fernandes-Alnemir, Teresa

APPLICANT: Litwack, Gerald

APPLICANT: Armstrong, Robert

APPLICANT: Tomaseilli, Kevin

TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,

TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,220

FILING DATE: 14-JUN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/618,408

FILING DATE: 19-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2165

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

TOPOLOGY: linear

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..84

OTHER INFORMATION: /note="human FADD"

US-08-665-220-64

Query Match 20.3%; Score 52; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLRYVSGDLFSMLLEQNDLEPGHTELLRELLASLRRLDLRRVDFFA 132
DB 33 KRKLRYVSGDLFSMLLEQNDLEPGHTELLRELLASLRRLDLRRVDFFA 84

RESULT 15
US-09-291-692-64
Sequence 64, Application US/09291692
Patent No. 6287795

GENERAL INFORMATION:

APPLICANT: Alnemir, Emaad S.

APPLICANT: Fernandes-Alnemir, Teresa

APPLICANT: Litwack, Gerald

APPLICANT: Armstrong, Robert

APPLICANT: Tomaseilli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED AND BERRY

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: Use

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/291,692

FILING DATE: 04-13-1999

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Christensen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..84

OTHER INFORMATION: /note="human FADD"

US-09-291-692-64

Query Match 20.3%; Score 52; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLRYVSGDLFSMLLEQNDLEPGHTELLRELLASLRRLDLRRVDFFA 132
DB 33 KRKLRYVSGDLFSMLLEQNDLEPGHTELLRELLASLRRLDLRRVDFFA 84

Search completed: June 19, 2003, 10:53:03
Job time : 27 secs

OS	Homo sapiens.
XX	
XX	WC9703998-A1.
XX	
PD	06-FEB-1997.
XX	
XX	14-JUN-1996;
XX	96WO-US10521.
XX	
PR	16-APR-1996;
PR	96ILT-0117932.
PR	16-JUL-1995;
PR	95ILT-0114615.
PR	17-AUG-1995;
PR	95ILT-0118986.
PR	14-SEP-1995;
PR	95ILT-0115319.
PR	27-SEP-1995;
XX	95ILT-0116588.
XX	
PA	(WEIN) WEINMUEZEL H.
PA	(YEDA) YEDA RES & DEV CO LTD

XX Boldin M, Golitsev YV, Goncharov T, Wallach D;
 XX WPI, 1997-132570/12.
 DR N-PSDB; AAT01397.
 XX
 PT New DNA encoding MACH protein that interacts with MORT-1 protein
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.
 XX
 PS Disclosure; Page 102-103; 163pp; English.

CC This sequence represents the mediator of cellular toxicity (MORT-1)
 CC protein. This sequence is bound by the protein of the invention (see
 CC AAM1892), designated MACH. MORT-1 binds to the FAS ligand receptor
 CC (FAS-R) death domain region, and triggers part of the cell death
 CC signalling cascade in mammalian cells. Vectors containing MACH, the MACH
 CC protein, and antibodies (Ab) against it are used to modulate the effect
 CC of FAS-R ligand or TNF on cells that carry FAS-R or p55-R. This is
 CC specifically for treating tumours, HIV-infected cells or other diseased
 CC cells, by control of apoptosis/programmed cell death. The MACH protein is
 CC a mediator of the cell death pathway initiated by TNF and FAS-R binding,
 CC i.e. it mimics or enhances the effect of MORT-1 where increased
 CC cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases
 CC of septic shock, graft rejection and acute hepatitis, sequences encoding
 CC antisense molecules or ribozymes, or Ab against MACH, are used.
 CC Compounds that inhibit MACH are potentially useful for controlling MACH
 CC activity e.g. in cases of autoimmune disease, oligodendrocyte death in
 CC multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can
 CC also be used to isolate and characterise other proteins and receptors
 CC involved in signalling and for Ab production. The Ab can be used to
 CC purify the new proteins and for diagnosis of conditions involving
 CC abnormal function of FAS-R mediated cellular effects.

XX Sequence 256 AA;

Query Match 100.0%; Score 256; DB 18; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.1e-233;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNAPCRFGGGLGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 60
 DB 1 VNAPCRFGGGLGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 60
 QY 61 SLSSESELELKFCLGRRVYKRLERVOGSLDFSMLEQNDLEPGHTELLRELLASLR 120
 DB 61 SLSSESELELKFCLGRRVYKRLERVOGSLDFSMLEQNDLEPGHTELLRELLASLR 120
 QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDMRRRLARQLKVSPTKIDSIEDR 180
 DB 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDMRRRLARQLKVSPTKIDSIEDR 180
 QY 181 YPNLTERVERRESLRIKNTKEKENATVAHLVGLALSCOMNLVADLYOEVOQARDLQNSGA 240
 DB 181 YPNLTERVERRESLRIKNTKEKENATVAHLVGLALSCOMNLVADLYOEVOQARDLQNSGA 240
 QY 241 MSPMSWNSDASTSEAS 256
 DB 241 MSPMSWNSDASTSEAS 256

RESULT 2
 AAR98346
 ID AAR98346 standard; Protein; 256 AA.

XX AAR98346;

XX 13-SEP-1996 (first entry)

XX MORT-1 modulator of FAS receptor.

XX MORT-1, HFL, FAS/APOL receptor; FAS-R; tumour; cancer; HIV;
 KM mediator of receptor toxicity; gene therapy.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Domain 160..221
 FT /Label= Death domain

XX W09618641-A1.

XX 20-JUN-1996.

XX 14-DEC-1995; 95MO-US16542.

XX 16-JUL-1995; 95IL-0114615.

XX 15-DEC-1994; 94IL-0112022.

XX 19-FEB-1995; 95IL-0112692.

XX (WEIN/) WEINMURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.

XX Boldin M, Mett I, Varfolomeev E, Wallach D;

XX WPI, 1996-300569/30.

XX N-PSDB; AAT30372.

XX MORT-1 protein capable of interacting with FAS-R intracellular
 PT domain - useful for modulating FAS-R ligand effect on cells and
 PT treating, e.g. tumour cells and HIV-infected cells

XX Claim 5; Fig 4; 72pp; English.

CC MORT-1 (AAR98346) (Mediator of Receptor Toxicity), also designated HFL,
 CC is a novel protein that binds to the intracellular domain (Fas-IC) of
 CC the Fas ligand receptor Fas-R (or FAS/APOL), and is capable of
 CC self-association and can activate cell cytotoxicity on its own.
 CC Recombinant MORT-1 can be obtd. from host cells transformed with a
 CC vector carrying a cDNA clone (AAT30372) isolated from HeLa cells.
 CC MORT-1 can be used to modulate the Fas-R ligand on cells carrying
 CC an Fas-R. It can also be used to treat tumour cells or HIV-infected
 CC cells, or to raise antibodies.

XX Sequence 256 AA;

Query Match 99.6%; Score 255; DB 17; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.8e-232;
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NOAPECRFGGGLGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 61

DB 2 NOAPECRFGGGLGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 61

QY 62 SLSSESELELKFCLGRRVYKRLERVOGSLDFSMLEQNDLEPGHTELLRELLASLR 121

DB 62 SLSSESELELKFCLGRRVYKRLERVOGSLDFSMLEQNDLEPGHTELLRELLASLR 121

QY 122 DLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDMRRRLARQLKVSPTKIDSIEDR 181

DB 122 DLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDMRRRLARQLKVSPTKIDSIEDR 181

QY 182 YPNLTERVERRESLRIKNTKEKENATVAHLVGLALSCOMNLVADLYOEVOQARDLQNSGA 241

DB 182 YPNLTERVERRESLRIKNTKEKENATVAHLVGLALSCOMNLVADLYOEVOQARDLQNSGA 241

QY 242 SPMMSWNSDASTSEAS 256

DB 242 SPMMSWNSDASTSEAS 256

RESULT 3
 AAY51329
 ID AAY51329 standard; Protein; 208 AA.

AC AAV51329;
 XX 19-APR-2000 (first entry)
 DT Human FADD protein.
 XX FADD; human; antisense; inhibitor; Fas-associated death domain.
 XX Homo sapiens.
 OS US6015712-A.
 PN 18-JAN-2000
 XX 19-JUL-1999; 99US-0357072.
 XX 19-JUL-1999; 99US-0357072.
 PR 19-JUL-1999; 99US-0357072.
 XX (ISIS-) ISIS PHARM INC.
 PA Montia BP, Covert LM, Baker BF, Zhang H;
 PI WPI: 2000-126316/11.
 DR N-PSDB; AA244745.
 XX Antisense oligonucleotides, useful for inhibiting human Fas-associated
 PT death domain (FADD) expression are targeted to the 3' untranslated
 PT region of the FADD gene
 XX Example 13; Column 43-46; 37pp; English.
 PS This invention describes novel antisense oligonucleotides (OGNs) (1)
 CC 8-20 nucleotides in length that specifically hybridize with and inhibit
 CC nucleic acids encoding human Fas-associated death domain (FADD),
 CC targeted to the 3' untranslated region (3'UTR). (1) can be used to treat
 CC animals, especially humans, suspected of having or being prone to a
 CC disease or condition associated with FADD expression. This sequence
 CC represents the human FADD protein described in the method of the
 CC invention.
 XX Sequence 208 AA;
 SQ
 Query Match 81.2%; Score 208; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-188;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 49 MDPFVYLHSVSSSSSELTEKELCGRVYKRLERVOGSLDFSMLEQNDEPGHT 108
 DB 1 MDPFVYLHSVSSSSSELTEKELCGRVYKRLERVOGSLDFSMLEQNDEPGHT 60
 QY 109 ELRELRLASLRHHDLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRLAROLK 168
 DB 61 ELRELRLASLRHHDLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRLAROLK 120
 QY 169 VSDPTIDSIDERYPRNLTERRPRESIRIKNTEKENATVAHVLGALRSCOMNVADLVQEV 228
 DB 121 VSDPTIDSIDERYPRNLTERRPRESIRIKNTEKENATVAHVLGALRSCOMNVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
 DB 181 QOARDLQNRSGAMSPMNSDASTSEAS 208
 RESULT 4
 AAM03653
 ID AAM03653 standard; Protein; 208 AA.
 AC AAM03653;
 XX 22-FEB-1997 (first entry)
 DT FADD (Fas-associated protein with novel death domain) protein..
 XX

KW Human; FADD; Fas-associated protein with novel death domain;
 KW apoptosis; Fas receptor; death domain; gene therapy; antibody;
 KW immunosassay; drug screening; diagnostic; AIDS; antiinflammatory;
 KW antitumour; cerebroprotective; neuroprotective.
 XX Homo sapiens.
 OS
 XX Key
 XX Region
 FT 1.125 "N-terminal fragment, inducing apoptosis but
 FT /note- "not binding to Fas receptor"
 FT Region
 FT 35..208
 FT /note- "C-terminal active fragment"
 FT Region
 FT 41..208
 FT /note- "C-terminal active fragment"
 FT Region
 FT 42..208
 FT /note- "Fas receptor-binding NFD-2 polypeptide"
 FT Region
 FT 61..208
 FT /note- "Fas receptor-binding NFD-3 polypeptide"
 FT Region
 FT 80..208
 FT /note- "Fas receptor-binding NFD-4 polypeptide"
 FT Misc-difference 121
 FT /note- "Altered to Asn in FADDmt mutant"
 FT Domain
 FT 111..177
 FT /note- "Death domain"
 XX W09631603-A2.
 XX 10-OCT-1996.
 XX 28-FEB-1996; 96MO-US02857.
 XX 18-MAY-1995; 95US-0443982.
 XX 03-APR-1995; 95US-0416379.
 XX (UNMI) UNIV MICHIGAN.
 XX Dixit VM, O'Rourke K;
 PI WPI: 1996-465026/46.
 DR N-PSDB; AAT39397.
 XX FADD protein that binds to cytoplasmic region of Fas receptor - for
 PT identifying inhibitors of Fas-associated apoptosis useful for
 PT treating e.g. AIDS, leukaemia, stroke, etc
 XX Example 1; Fig 2A-B; 96pp; English.
 PS The sequence corresponds to FADD (Fas-associated protein with novel
 CC death domain), which binds the cytoplasmic region of a Fas receptor,
 CC and modulates apoptosis induced by activation of the receptor by
 CC ligand binding. The FADD cDNA has been isolated using a yeast
 CC two-hybrid system to screen for proteins interacting with the Fas
 CC cytoplasmic domain. The protein contains a death domain, with
 CC interacts with the death domain of Fas. Mutation of Val-121 to
 CC Asn in mutant FADDmt disrupts binding and/or signalling properties.
 CC C-terminal polypeptides NFD-2, NFD-3 and NFD-4 bind the Fas receptor
 CC cytoplasmic domain in vitro. An N-terminal fragment induces
 CC apoptosis but does not bind the Fas receptor. The encoding DNA may
 CC be used in gene therapy, and the protein or a corresponding antibody
 CC may be used to screen for agents modulating FADD pathway cellular
 CC functions and Fas-associated apoptosis, for use in therapy of e.g.
 CC AIDS, inflammation, leukaemia, myocardial infarction, degenerative
 CC disease, etc.
 XX Sequence 208 AA;
 SQ
 Query Match 68.8%; Score 176; DB 17; Length 208;
 Best Local Similarity 100.0%; Pred. No. 6.3e-158;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 81 KRKLERYVSGDLDFSMLEQNDEPGHRELRLASLRHHDLRRVDFEAGAAAGAP 140
 II

DB 33 KRLEEVOSGLDFSMLEQNDLEPGHTELLRELLASLRHDLRRVDFEAGAAGAP 92
QY 141 GEEDLCAAFNVICDNGKMRRLAROLKYSDFKIDSIEDRYPNLTERVESIRIKNTE 200
DB 93 GEEDLCAAFNVICDNGKMRRLAROLKYSDFKIDSIEDRYPNLTERVESIRIKNTE 152
QY 201 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 256
DB 153 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 208

RESULT 5
AAM96154
ID AAM96154 standard; Protein; 208 AA.
AC AAM96154;
XX
XX
DT 27-APR-1999 (first entry)
XX
XX
DE Human FADD protein.
XX
XX
XX FIP; FADD interacting protein; FADD; Fas-associated protein with a
XX novel death domain; cell death; apoptosis; Alzheimer's disease;
XX Acquired Immune Deficiency Syndrome; AIDS; muscular dystrophy;
XX amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasma;
XX protozoa; neoplasia; dysplasia; hyperplasia.
XX
XX Homo sapiens.
XX
XX MO9900499-A1.
XX
XX PD 07-JAN-1999.
XX
XX PF 26-JUN-1998; 98MO-US13320.
XX
XX PR 03-JUN-1998; 98US-0087886.
XX
XX PR 26-JUN-1997; 97US-0050792.
XX
XX PA (CHTR) CHIRON CORP.
XX
XX PI Chen TT, Williams LT;
XX
XX DR WPI; 1999-095745/08.
XX
XX DR N-PSDB; AAX08910.
XX
XX PT New FADD (Fas-associated protein with a novel death
XX domain)-Interacting Protein - useful for inducing or preventing
XX apoptosis in a cell, to aid in controlling apoptosis-related
XX diseases
XX
XX PS Disclosure; Page 47; 58pp; English.

CC An epitope of human FADD (Fas-associated protein with a novel
CC death domain)-Interacting protein (FIP protein) comprising amino
CC acids 348-727 of the protein described in AAM96153, can be used to
CC induce or prevent apoptosis in a cell. Specifically, decreasing the
CC levels of FIP348-727 prevents apoptosis. This is useful in cells
CC which are dying prematurely, eg: Alzheimer's disease, Acquired
CC Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic
CC lateral sclerosis (and other muscle wasting diseases), autoimmune
CC diseases, and diseases where cells are infected with a pathogen
CC (virus, bacteria, fungus, mycoplasma or protozoa). Increasing the
CC levels of FIP 348-727 induces apoptosis which is useful in cells
CC suffering from neoplasias, dysplasias, hyperplasias, or their
CC symptoms. Purified and isolated FIP subgenomic polynucleotides are
CC useful as primers to obtain more copies of the nucleotides, and as
CC probes that identify wild-type or mutant coding sequences. They are
CC also useful for expressing FIP mRNA, proteins or fusion proteins,
CC and in the generation of FIP antisense oligonucleotides and
CC ribozymes. They are also useful in expression constructs and in
CC gene delivery vehicles (optionally in combination with a condensing
CC agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
CC (including variants), FIP-specific ribozymes or single chain

CC antibodies into eukaryotic cells. This is the human FADD protein.
CC Human FIP protein binds to amino acids 1-110 of this sequence.
XX
SQ Sequence 208 AA;
QY
DB 81 KRLEEVOSGLDFSMLEQNDLEPGHTELLRELLASLRHDLRRVDFEAGAAGAP 140
DB 33 KRLEEVOSGLDFSMLEQNDLEPGHTELLRELLASLRHDLRRVDFEAGAAGAP 92
QY 141 GEEDLCAAFNVICDNGKMRRLAROLKYSDFKIDSIEDRYPNLTERVESIRIKNTE 200
DB 93 GEEDLCAAFNVICDNGKMRRLAROLKYSDFKIDSIEDRYPNLTERVESIRIKNTE 152
QY 201 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 256
DB 153 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 208

RESULT 6
AAB84804
ID AAB84804 standard; Protein; 208 AA.
AC AAB84804;
XX
XX
DT 12-JUL-2001 (first entry)
XX
XX
DE Human FADD prodomain.
XX
XX
XX NF-kappaB; JNK; apoptosis; death effector domain; DED.
XX
XX Homo sapiens.
XX
XX OS
XX PN US6207458-B1.
XX
XX PD 27-MAR-2001.
XX
XX PF 07-MAY-1998; 98US-0074044.
XX
XX PR 07-MAY-1998; 98US-0074044.
XX
XX PA (UNIV) UNIV WASHINGTON.
XX
XX PI Chaudhary PM, Hood L;
XX
XX DR WPI; 2001-342087/36.
XX
XX

PT Testing candidate compound affecting cellular NF-kappaB JNK, apoptosis
PT activity by comparing cell activity in presence and absence of
PT proteinaceous species having two death effector domain and test
PT compound
XX
XX PS Disclosure; Column 51-52; 62pp; English.

CC The present invention relates to testing candidate compounds to
CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
CC The method involves the use of 2 death effector domains (DED). The
CC compounds identified by the invention have therapeutic
CC applications and are useful for regulating cellular NF-kappaB, JNK
CC and apoptosis activity. The assay is useful for identifying
CC pharmacological agents or lead compounds generally involved in
CC assaying for compounds which regulate or modulate a cell activity.
CC The present sequence is a prodomain used in the invention.
XX
XX

SQ Sequence 208 AA;

Query Match 68.8%; Score 176; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.3e-158;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRKLERSVSGDLEFMSMLEONDLBPGHTELLRELLASLRHDLRRVDFEAGAAAGAP 140
 DB 33 KRKLERSVSGDLEFMSMLEONDLBPGHTELLRELLASLRHDLRRVDFEAGAAAGAP 92
 OY 141 GEEDLCAAFNYICNVGCDKMRRLAROLKVSPTKIDSIDRYPRNLTERVRESLRKWKTE 200
 DB 93 GEEDLCAAFNYICNVGCDKMRRLAROLKVSPTKIDSIDRYPRNLTERVRESLRKWKTE 152
 OY 201 KENATVAHLVGLASCOMNLVADLVQEVQARDLQNSGASPMWSNDSASTSEAS 256
 DB 153 KENATVAHLVGLASCOMNLVADLVQEVQARDLQNSGASPMWSNDSASTSEAS 208

RESULT 7
 AAM87491
 ID AAM87491 standard; Protein; 201 AA.
 AC AAM87491;
 XX 12-FEB-1999 (first entry)
 DE Amino acid sequence of MOR1 isoform MOR1del21 from NTERA2 cells.

XX MOR1; MOR1del21; NTERA2; CNS; isoform; death domain; Fas/APOL;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.
 XX Homo sapiens.
 OS
 XX MO849297-A1.
 XX 05-NOV-1998.
 PD 14-APR-1998; 98WO-US07439.
 FF 25-APR-1997; 97US-0044835.
 PR (AMHP) AMERICAN HOME PROD CORP.
 XX Blingham BW, Birsan C, Wood AT, Young KH;
 PI WPI; 1999-009424/01.
 DR N-PSDB; AAV71928.

XX Human, neuronal MOR1 isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 PS Claim 5; Pages 26-27; 31pp; English.
 XX This represents the amino acid sequence of a MOR1 isoform MOR1del21.
 CC The encoding cDNA was isolated from NTERA2 cells and deposited under the
 CC accession number ATCC 209013. The cDNA has a 21 base pair deletion as
 CC compared to the published MOR1 sequence (bp 172-192 of the coding
 CC sequence). The invention relates to three MOR1 nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the
 CC death domain of Fas/APOL. The MOR1 isoforms can also interact with the
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.

XX Sequence 201 AA;

Query Match 44.5%; Score 114; DB 20; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2.2e-99;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICNVGCDKMRRLAROLKVSPT 172

DB 58 ELASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICNVGCDKMRRLAROLKVSPT 117
 OY 173 KIDSIEDRYPRNLTERVRESLRKWKTEKENATVAHLVGLASCOMNLVADLVQ 226
 DB 118 KIDSIEDRYPRNLTERVRESLRKWKTEKENATVAHLVGLASCOMNLVADLVQ 171

RESULT 8
 AAM87493
 ID AAM87493 standard; Protein; 208 AA.
 AC AAM87493;
 XX 12-FEB-1999 (first entry)
 DE Amino acid sequence of MOR1 isoform MOR1G173A from human brain.

XX MOR1; MOR1G173A; NTERA2; CNS; isoform; death domain; Fas/APOL;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.
 XX Homo sapiens.
 OS
 XX MO849297-A1.
 XX 05-NOV-1998.
 PD 14-APR-1998; 98WO-US07439.
 FF 25-APR-1997; 97US-0044835.
 PR (AMHP) AMERICAN HOME PROD CORP.
 XX Blingham BW, Birsan C, Wood AT, Young KH;
 PI WPI; 1999-009424/01.
 DR N-PSDB; AAV71930.

XX Human, neuronal MOR1 isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 PS Claim 7; Pages 30-31; 31pp; English.
 XX This represents the amino acid sequence of a MOR1 isoform MOR1G173A.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209019. The cDNA has a nucleotide substitution (G
 CC to A) at basepair position 173 of the published MOR1 coding sequence.
 CC The invention relates to three MOR1 nucleic acid isoforms (AAV71928 to
 CC AAV71930) that encode proteins which can interact with the death domain
 CC of Fas/APOL. The MOR1 isoforms can also interact with MACH alpha1 or
 CC other members of the ICE/Ced3 (Caspase) family of proteins. The
 CC transcript isoforms, together with their encoded proteins are useful as
 CC screening agents in diagnosing CNS diseases, and in discovering
 CC CNS-specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.

XX Sequence 208 AA;

Query Match 44.5%; Score 114; DB 20; Length 208;
 Best Local Similarity 100.0%; Pred. No. 2.3e-99;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 HTELLRELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICNVGCDKMRRLARQ 166
 DB 59 HTELLRELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICNVGCDKMRRLARQ 118

OY 167 LKVSPTKIDSIDRYPRNLTERVRESLRKWKTEKENATVAHLVGLASCOMNL 220
 DB 119 LKVSPTKIDSIDRYPRNLTERVRESLRKWKTEKENATVAHLVGLASCOMNL 172

PN W09625941-A1.
 XX
 PD 29-AUG-1996.
 XX
 PF 15-FEB-1996; 96WO-US02326.
 XX
 PR 13-SEP-1995; 95IL-0115289.
 PR 22-FEB-1995; 95IL-0112742.
 XX
 PA (WEIN/) WEINMURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Boidin MP, Goncharov TM, Mett I, Pancer Z, Varfolomeev EE;
 PI Wallach D;
 XX WPI: 1996-402125/40.
 DR
 XX
 PT Modulator of regulatory cellular events mediated by "death domain"
 PT contg. regulatory proteins - useful for modulating functions
 PT mediated in cells by proteins contg the death domain
 XX
 PS Claim 9; Fig 1; 74pp: English.
 CC
 CC AAM00210 shows the death domain of the MORT-1, which binds to the
 CC intracellular portion of the human Fas-ligand receptor (FAS-R). The
 CC death domain (DD) of FAS-R, p55 tumour necrosis factor receptor
 CC (p55 TNF-R), nerve growth factor receptor (NGF-R) and ankyrin 1 are also
 CC given (see AAM00206 and AAM00208-W00210). These Dds are used to identify
 CC compounds capable of modulating activity of the regulatory proteins
 CC (p55, NGF, TNF and FAS-R ligand, MORT-1) via interaction with the Dds.
 CC Such modulators which may be antibodies, antisense sequences or
 CC ribozymes (which can affect the cellular mRNA sequences encoding the
 CC proteins) and are useful for modulation of effects of the regulatory
 CC proteins within the cell. Tumour cells, HIV-infected cells or other
 CC diseased cells can be treated by targeting the cells with animal viral
 CC vectors encoding the modulators and a viral surface antigen capable of
 CC binding to a specific receptor. The Dds are characterised by having
 CC groups of common amino acid residues Trp, Ala, Asp, Glu, Thr, Arg and
 CC Tyr within locations that can be aligned to show homology.
 XX
 SQ Sequence 62 AA:
 Query Match 24.2%; Score 62; DB 17; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1e-50;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 160 WRRLAROLKVSPTKIDSTEDRRPRLTERVRESLIRKNTKEKNTVAHLVGLALSSCOMN 219
 DB 1 WRRLAROLKVSPTKIDSTEDRRPRLTERVRESLIRKNTKEKNTVAHLVGLALSSCOMN 60
 OY 220 LV 221
 DB 61 LV 62
 RESULT 12
 AAB84800
 ID AAB84800 standard; Protein; 83 AA.
 AC AAB84800;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE FADD death effector domain 1.
 XX
 KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
 OS Homo sapiens.
 XX
 PN US6207458-B1.
 PD 27-MAR-2001.
 XX

PF 07-MAY-1998; 98US-0074044.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIM) UNIV WASHINGTON.
 XX
 PI Chaudhary PM, Hood L;
 XX
 DR WPI: 2001-342087/36.
 XX
 PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
 PT activity by comparing cell activity in presence and absence of
 PT proteolaceous species having two death effector domain and test
 PT compound
 XX
 PS Claim 10; Column 45-47; 62pp; English.
 CC
 CC The present invention relates to testing candidate compounds to
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
 CC The method involves the use of 2 death effector domains (DED). The
 CC compounds identified by the invention have therapeutic
 CC applications and are useful for regulating cellular NFkappaB, JNK
 CC and apoptosis activity. The assay is useful for identifying
 CC pharmacological agents or lead compounds generally involved in
 CC assaying for compounds which regulate or modulate a cell activity.
 CC The present sequence is a death effector domain of the invention.
 XX
 SQ Sequence 83 AA:
 Query Match 19.9%; Score 51; DB 22; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.2e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 81 RKRLRVOSGLDFSLLEQNDLEPGHMLRELLASRRHDLRVDDFE 131
 DB 33 RKRLRVOSGLDFSLLEQNDLEPGHMLRELLASRRHDLRVDDFE 83
 RESULT 13
 AAB61115
 ID AAB61115 standard; protein; 83 AA.
 AC AAB61115;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Human FADD DED1 domain.
 XX
 KW Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KW Jun N-terminal kinase; JNK; apoptosis; Caspase-8 mutant;
 KW death effector domain; DED.
 XX
 OS Homo sapiens.
 XX
 PN US6160095-A.
 PD 12-DEC-2000.
 XX
 PF 24-AUG-1999; 99US-0382155.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIM) UNIV WASHINGTON.
 PA (STOM-) STOMERS INST MEDICAL RES.
 XX
 PI Hood L, Chaudhary PM;
 XX
 DR WPI: 2001-101569/11.
 XX
 PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PT nuclear factor-kappa B, Jun N-terminal Kinase and apoptosis activities,
 PT for therapeutic purposes
 XX

PS Example 8; Fig 11; 60pp; English.

XX The present sequence is a death effector domain (DED) of a protein

CC that has been shown to regulate the nuclear factor-kappa

CC B (NF-kB), Jun N-terminal kinase (JNK) and apoptosis pathways. It

CC is provided in a specification relating to novel mutants (D73A, L74A and

CC L75A) for Caspase-8 which are also useful for regulating NF-kB, JNK

CC and apoptosis activities. The Caspase-8 mutants are useful for

CC therapeutic purposes and in test methods or assays for determining

CC whether a candidate compound has a significant effect upon cell

CC activities, especially NF-kB, JNK and apoptosis, so as to facilitate the

CC discovery and/or design of therapeutic agents.

XX

SQ Sequence 83 AA;

Query Match 19.9%; Score 51; DB 22; Length 83;

Best Local Similarity 100.0%; Pred. No. 3.2e-40;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILLRVDPFE 131

DB 33 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILLRVDPFE 83

RESULT 14

ABB81755

ID ABB81755 standard; protein; 85 AA.

XX

AC ABB81755;

XX

DT 10-SEP-2002 (first entry)

XX

DE Tumour necrosis factor Fas associated death domain death effector domain.

XX

KW Tumour necrosis factor; receptor; TNFR-1; death domain; DED;

KM TNFR-1-D; Fas associated death domain; FADD; death effector domain;

KV protein co-ordinate data.

XX

OS Unidentified.

XX

PN US2002045578-A1.

XX

PD 18-APR-2002.

XX

PF 14-MAY-2001; 2001US-0854906.

XX

PR 22-MAY-2000; 2000US-206215P.

XX

PA (SURK/) SURKTS S F.

PA (XUGG/) XU G.

PA (LINL/) LIN L.

PA (TELL/) TELLIEZ J.

PA (HSUS/) HSU S.

XX

PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

XX

DR WPI; 2002-443412/47.

XX

PT Solution comprising tumor necrosis factor receptor 1 death domain,

PT useful for identifying potential inhibitor of tumor necrosis factor

PT receptor 1 death domain

XX

PS Disclosure; Fig 7; 49pp; English.

XX

CC The sequence represents the tumour necrosis Fas associated death domain

CC death effector domain (FADD DED). The invention relates to a novel

CC solution comprising a tumour necrosis factor receptor 1 death domain. The

CC solution is useful for identifying a potential inhibitor of TNFR-1-D,

CC for the design and selection of potent and selective inhibitors of TNF

CC signaling pathways, and for generating a three-dimensional structure for

CC an unknown molecule or molecular complex.

XX

SQ Sequence 85 AA;

Query Match 19.9%; Score 51; DB 23; Length 85;

Best Local Similarity 100.0%; Pred. No. 3.3e-40;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILLRVDPFE 131

DB 33 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILLRVDPFE 83

RESULT 15

AAW76623

ID AAW76623 standard; protein; 81 AA.

XX

AC AAW76623;

XX

DT 12-JUL-1999 (first entry)

XX

DE Human FADD protein fragment containing death effector domain.

XX

KW Death effector domain; human; murine; anti-apoptotic; treatment;

KM HIV infection; autoimmune disease; FADD protein.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT Misc-difference 6

FT /label= unknown

XX

PN DEL9713393-A1.

XX

PD 08-OCT-1998.

XX

PF 01-APR-1997; 97DE-1013393.

XX

PR 01-APR-1997; 97DE-1013393.

XX

PA (TSCH/) TSCHOPP J.

PA (APOT-) APOTTECH SA.

XX

PI Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;

PI Irmeler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;

PI Thome M, Tschopp J, Hoffmann K;

XX

DR WPI; 1998-532710/46.

XX

PT New DNA encoding for anti-apoptotic gene product - used to treat HIV

PT infections and autoimmune diseases

XX

PS Disclosure; Fig 2; 45pp; German.

XX

CC This invention describes novel human and mouse anti-apoptotic gene

CC products which contain at least one death effector domain. The products

CC of the invention are used in the treatment of HIV infections and

CC autoimmune diseases.

XX

SQ Sequence 81 AA;

Query Match 14.5%; Score 37; DB 19; Length 81;

Best Local Similarity 100.0%; Pred. No. 5.3e-27;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLAS 117

DB 33 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLAS 69

Search completed: June 19, 2003, 10:45:32

Job time : 36.secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:28:30 ; Search time 70 Seconds

(without alignments)
487,317 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302

Sequence: 1 VNOAPECRFGGCGILGPIGKR..... RSGAMSPMSNDSASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq.101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
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- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1302	100.0	256	18	AAW1894	Modulator of cellu
2	1299	99.8	256	17	AAW98346	MORT-1 modulator o
3	1047	80.4	208	21	AAW51329	Human FADD protein
4	1040	79.9	208	17	AAW03653	FADD (Fas-associat
5	1040	79.9	208	20	AAW96154	Human FADD protein
6	1040	79.9	208	22	AAW84804	Human FADD protein
7	1038	79.3	208	22	AAW61119	Human FADD. Homo
8	1038	79.0	208	20	AAW87493	Amino acid sequenc
9	985.5	75.7	201	20	AAW87492	Amino acid sequenc
10	982.5	75.5	201	20	AAW87491	Amino acid sequenc

11	719.5	55.3	205	22	AAW61900	Mouse apoptosis me
12	401	30.8	83	22	AAW84800	FADD death effecto
13	401	30.8	83	22	AAW61115	Human FADD DED1 do
14	401	30.8	85	23	AAW81755	Tumour necrosis fa
15	375	28.8	81	19	AAW76623	Human FADD protein
16	370.5	28.5	117	22	AAW61902	Mouse apoptosis me
17	349	26.6	88	22	AAW61901	Mouse apoptosis me
18	346	26.6	99	23	AAW81754	Tumour necrosis fa
19	318	24.4	62	17	AAW00210	Human MORT-1 prote
20	125.5	9.6	480	22	AAW06523	Mouse caspase 8 pr
21	122.5	9.4	239	22	AAW62302	Drosophila melanog
22	122	9.4	180	22	AAW84803	Human caspase 8 pr
23	122	9.4	180	22	AAW61118	Human caspase-8.
24	122	9.4	220	19	AAW75961	Human Caspase-8h.
25	122	9.4	235	18	AAW1892	MORT-1 binding pro
26	122	9.4	257	18	AAW31735	Cell death-associat
27	122	9.4	261	18	AAW1898	MACH isoform beta4
28	122	9.4	277	18	AAW1893	MACH isoform beta3
29	122	9.4	464	18	AAW1895	MACH isoform alpha
30	122	9.4	479	18	AAW31523	Human Caspase-8.
31	122	9.4	479	18	AAW1891	Interleukin-1 beta
32	122	9.4	479	19	AAW75963	Human caspase-8.
33	122	9.4	479	22	AAW0605	Human caspase-8 L7
34	117	9.0	479	22	AAW84812	Human caspase-8 L7
35	117	9.0	479	22	AAW84813	Human caspase-8 mu
36	117	9.0	479	22	AAW61127	Human Caspase-8 mu
37	117	9.0	479	22	AAW61128	Human Caspase-8 mu
38	116.5	8.9	291	21	AAW67420	Usurpin-gamma poly
39	116.5	8.9	1975	22	AAW62094	Drosophila melanog
40	116	8.9	81	19	AAW75962	Human Caspase-8L1
41	116	8.9	83	22	AAW84796	Caspase 8 death ef
42	116	8.9	83	22	AAW61111	Human caspase-8 DE
43	116	8.9	110	22	AAW30630	Peptide #3310 enco
44	116	8.9	110	22	AAW35830	Peptide #3336 enco
45	116	8.9	110	22	AAW21245	Protein #3244 enco

ALIGNMENTS

RESULT 1

ID AAW1894 standard; Protein; 256 AA.

XX AAW1894;

XX 29-OCT-1997 (first entry)

XX Modulator of cellular toxicity (MORT-1).

XX MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death;

XX antibody; FAS ligand receptor; FAS-R; death domain region; septic shock;

XX tumour necrosis factor; tumour; HIV-1 infection; oligodendrocyte death;

XX apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis;

XX autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;

XX TNF; Therapy.

XX Homo sapiens.

XX MO9703998-A1.

XX 06-FEB-1997.

XX 14-JUN-1996; 96WO-US10521.

XX 16-APR-1996; 96IL-0117932.

XX 17-AUG-1995; 95IL-0114615.

XX 14-SEP-1995; 95IL-0114986.

XX 27-SEP-1995; 95IL-0115319.

XX (WEIN/) WEINMURZEL H.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Boldin M, Goltsev IV, Goncharov T, Wallach D;
 XX MPI: 1997-132570/12.
 DR N-PSDB; AAT61397.
 XX
 XX New DNA encoding MACH protein that interacts with MORT-1 protein -
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.
 XX
 PS Disclosure; Page 102-103; 163pp; English.
 XX
 CC This sequence represents the mediator of cellular toxicity (MORT-1)
 CC protein. This sequence is bound by the protein of the invention (see
 CC AAT61892), designated MACH. MORT-1 binds to the FAS ligand receptor.
 CC (FAS-R) death domain region, and triggers part of the cell death
 CC signalling cascade in mammalian cells. Vectors containing MACH, the MACH
 CC protein, and antibodies (Ab) against it are used to modulate the effect
 CC of FAS-R ligand or TNF on cells that carry FAS-R or p53-R. This is
 CC specifically for treating tumours, HIV-infected cells or other diseased
 CC cells, by control of apoptosis/programmed cell death. The MACH protein is
 CC a mediator of the cell death pathway initiated by TNF and FAS-R binding,
 CC i.e. it mimics or enhances the effect of MORT-1 where increased
 CC cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases
 CC of septic shock, graft rejection and acute hepatitis, sequences encoding
 CC antisense molecules or ribozymes, or Ab against MACH, are used.
 CC Compounds that inhibit MACH are potentially useful for controlling MACH
 CC activity e.g. in cases of autoimmune disease, oligodendrocyte death in
 CC multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can
 CC also be used to isolate and characterise other proteins and receptors
 CC involved in signalling and for Ab production. The Ab can be used to
 CC purify the new proteins and for diagnosis of conditions involving
 CC abnormal function of FAS-R mediated cellular effects.
 CC
 XX
 SQ Sequence 256 AA:
 Query Match 100.0%; Score 1302; DB 18; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.8e-125;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNQAECRRGGGILPLGKRRDLARASEPRTGARRAGOPPPADPADPPLVLLHSYS 60
 Db 1 VNQAECRRGGGILPLGKRRDLARASEPRTGARRAGOPPPADPADPPLVLLHSYS 60
 QY 61 SLSSESELTELKFLCIGRVYRKRLERVOGGLDFSMLEQNDLEPGHTELLRELLASLR 120
 Db 61 SLSSESELTELKFLCIGRVYRKRLERVOGGLDFSMLEQNDLEPGHTELLRELLASLR 120
 QY 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDNVGMKWRRLARQLKVSDFRKIDSIER 180
 Db 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDNVGMKWRRLARQLKVSDFRKIDSIER 180
 QY 181 YPRNLTERRRESLRIRKNTKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 Db 181 YPRNLTERRRESLRIRKNTKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 QY 241 MSPMSMNSDASTSEAS 256
 Db 241 MSPMSMNSDASTSEAS 256
 RESULT 2
 AAR98346
 ID AAR98346 standard; Protein; 256 AA.
 XX
 AC AAR98346;
 XX
 DT 13-SEP-1996. (first entry)
 XX
 DE MORT-1 modulator of FAS receptor.
 XX
 KM MORT-1; HFL: FAS/APOL receptor; FAS-R; tumour; cancer; HIV;
 mediator of receptor toxicity; gene therapy.

XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Domain 160..221
 FT /Label= Death domain
 PN W09618641-A1.
 XX
 XX 20-JUN-1996.
 PD
 XX
 XX 14-DEC-1995; 95WO-US16542.
 PF
 XX
 PR 16-JUL-1995; 95IL-0114615.
 PR 15-DEC-1994; 94IL-0112022.
 PR 19-FEB-1995; 95IL-0112692.
 XX
 PA (WEIN/) WEINMUTZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Boldin M, Mett I, Varfolomeev E, Wallach D;
 DR MPI: 1996-300569/30.
 DR N-PSDB; AAT30372.
 XX
 PT MORT-1 protein capable of interacting with FAS-R intracellular
 PT domain - useful for modulating FAS-R ligand effect on cells and
 PT treating, e.g. tumour cells and HIV-infected cells
 XX
 PS Claim 5; Fig 4; 72pp; English.
 XX
 CC MORT-1 (AAR98346) (Mediator of Receptor Toxicity), also designated HFL,
 CC is a novel protein that binds to the intracellular domain (Fas-IC) of
 CC the Fas ligand receptor Fas-R (or Fas/APOL), and is capable of
 CC modulating the function of Fas-R. MORT-1 is also capable of
 CC self-association and can activate cell cytotoxicity on its own.
 CC Recombinant MORT-1 can be obtd. from host cells transformed with a
 CC vector carrying a cDNA clone (AAT30372) isolated from HeLa cells.
 CC MORT-1 can be used to modulate the Fas-R ligand on cells carrying
 CC an Fas-R. It can also be used to treat tumour cells or HIV-infected
 CC cells, or to raise antibodies.
 CC
 XX
 SQ Sequence 256 AA:
 Query Match 99.8%; Score 1299; DB 17; Length 256;
 Best Local Similarity 99.6%; Pred. No. 5.7e-125;
 Matches 255; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNQAECRRGGGILPLGKRRDLARASEPRTGARRAGOPPPADPADPPLVLLHSYS 60
 Db 1 VNQAECRRGGGILPLGKRRDLARASEPRTGARRAGOPPPADPADPPLVLLHSYS 60
 QY 61 SLSSESELTELKFLCIGRVYRKRLERVOGGLDFSMLEQNDLEPGHTELLRELLASLR 120
 Db 61 SLSSESELTELKFLCIGRVYRKRLERVOGGLDFSMLEQNDLEPGHTELLRELLASLR 120
 QY 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDNVGMKWRRLARQLKVSDFRKIDSIER 180
 Db 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDNVGMKWRRLARQLKVSDFRKIDSIER 180
 QY 181 YPRNLTERRRESLRIRKNTKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 Db 181 YPRNLTERRRESLRIRKNTKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 QY 241 MSPMSMNSDASTSEAS 256
 Db 241 MSPMSMNSDASTSEAS 256
 RESULT 3
 AAT51329
 ID AAT51329 standard; Protein; 208 AA.
 XX

AC AAY51329;
 XX 19-APR-2000 (first entry)
 XX Human FADD protein.
 DE Human FADD protein.
 XX FADD; human; antisense; inhibitor; Fas-associated death domain.
 XX Homo sapiens.
 OS US6015712-A.
 XX 18-JAN-2000.
 XX 19-JUL-1999; 99US-0357072.
 XX 19-JUL-1999; 99US-0357072.
 XX 19-JUL-1999; 99US-0357072.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Covert LM, Baker BF, Zhang H;
 XX WPI; 2000-126316/11.
 DR N-PSDB; AAZ44745.
 XX Antisense oligonucleotides, useful for inhibiting human Fas-associated
 PT death domain (FADD) expression are targeted to the 3' untranslated
 PT region of the FADD gene -
 XX Example 13; Column 43-46; 37pp; English.
 XX This invention describes novel antisense oligonucleotides (OGNs) (1)
 CC 8-30 nucleotides in length that specifically hybridize with and inhibit
 CC nucleic acids encoding human Fas-associated death domain (FADD).
 CC Targeted to the 3' untranslated region (3'UTR). (1) can be used to treat
 CC animals, especially humans, suspected of having or being prone to a
 CC disease or condition associated with FADD expression. This sequence
 CC represents the human FADD protein described in the method of the
 CC invention.
 XX Sequence 208 AA;
 SQ

Query Match 80.4%; Score 1047; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.3e-99;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 MDPEVYLHSSVSSISSELELKFICGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108
 DB 1 MDPEVYLHSSVSSISSELELKFICGRVYKRLERVOGSLDFSMLEQNDLEPGHT 60
 QY 109 ELRELALSLRRHDLRRVDFEAGAAAGAAAGGEEEDLCAPNVICDNYGKDMRLAROLK 168
 DB 61 ELRELALSLRRHDLRRVDFEAGAAAGAAAGGEEEDLCAPNVICDNYGKDMRLAROLK 120
 QY 169 VSDRTIDIEDIRPNTLTERPRESIRIKTKTEKEKNAVYAHVLGALRSCOMLVADLYOEY 228
 DB 121 VSDRTIDIEDIRPNTLTERPRESIRIKTKTEKEKNAVYAHVLGALRSCOMLVADLYOEY 180
 QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
 DB 181 QOARDLQNRSGAMSPMNSDASTSEAS 208

RESULT 4
 AAW03653
 ID AAW03653 standard; Protein; 208 AA.
 XX AAW03653;
 AC AAW03653;
 XX 22-FEB-1997 (first entry)
 DT 22-FEB-1997 (first entry)
 XX FADD (Fas-associated protein with novel death domain) protein.
 DE FADD (Fas-associated protein with novel death domain) protein.
 XX

KW Human; FADD; Fas-associated protein with novel death domain;
 KW apoptosis; Fas receptor; death domain; gene therapy; antibody;
 KW immunosay; drug screening; diagnostic; AIDS; antiinflammatory;
 KW antitumor; cerebroprotective; neuroprotective.
 XX Homo sapiens.
 OS
 FH Key
 FT Region
 FT Location/Qualifiers
 FT 1..125 "N-terminal fragment, inducing apoptosis but
 FT /note= "N-terminal fragment, inducing apoptosis but
 FT not binding to Fas receptor"
 FT 35..208
 FT /note= "C-terminal active fragment"
 FT 41..208
 FT /note= "C-terminal active fragment"
 FT 42..208
 FT /note= "Fas receptor-binding NFD-2 polypeptide".
 FT 61..208
 FT /note= "Fas receptor-binding NFD-3 polypeptide".
 FT 80..208
 FT /note= "Fas receptor-binding NFD-4 polypeptide".
 FT /note= "Fas receptor-binding NFD-4 polypeptide".
 FT Misc-difference 121
 FT /note= "Altered to Asn in FADDmt mutant".
 FT 111..177
 FT Domain
 FT /note= "Death domain"
 PN W09631603-A2.
 PD 10-OCT-1996.
 XX 28-FEB-1996; 96MO-US02857.
 XX 18-MAY-1995; 95US-0443982.
 PR 03-APR-1995; 95US-0416379.
 XX (UNMI) UNIV MICHIGAN.
 PA Dixit VM, O'Rourke K;
 PI WPI; 1996-465026/46.
 DR N-PSDB; AAT39397.
 XX FADD protein that binds to cytoplasmic region of Fas receptor - for
 PT identifying inhibitors of Fas-associated apoptosis useful for
 PT treating e.g. AIDS, leukaemia, stroke, etc
 PT Example 1; Fig 2A-B; 96pp; English.
 PS The sequence corresponds to FADD (Fas-associated protein with novel
 CC death domain), which binds the cytoplasmic region of a Fas receptor,
 CC and modulates apoptosis induced by activation of the receptor by
 CC ligand binding. The FADD cDNA has been isolated using a yeast
 CC two-hybrid system to screen for proteins interacting with the Fas
 CC cytoplasmic domain. The protein contains a death domain with
 CC interacts with the death domain of Fas. Mutation of Val-121 to
 CC Asn in mutant FADDmt disrupts binding and/or signalling properties.
 CC C-terminal polypeptides NFD-2, NFD-3 and NFD-4 bind the Fas receptor
 CC cytoplasmic domain in vitro. An N-terminal fragment induces
 CC apoptosis but does not bind the Fas receptor. The encoding DNA may
 CC be used to screen for agents modulating FADD pathway cellular
 CC functions and Fas-associated apoptosis, for use in therapy of e.g.
 CC AIDS, inflammation, leukaemia, myocardial infarction, degenerative
 CC disease, etc.
 XX Sequence 208 AA;
 SQ

Query Match 79.9%; Score 1040; DB 17; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.7e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVYLHSSVSSISSELELKFICGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108
 DB 1 MDPEVYLHSSVSSISSELELKFICGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108
 QY 109 ELRELALSLRRHDLRRVDFEAGAAAGAAAGGEEEDLCAPNVICDNYGKDMRLAROLK 168
 DB 61 ELRELALSLRRHDLRRVDFEAGAAAGAAAGGEEEDLCAPNVICDNYGKDMRLAROLK 120
 QY 169 VSDRTIDIEDIRPNTLTERPRESIRIKTKTEKEKNAVYAHVLGALRSCOMLVADLYOEY 228
 DB 121 VSDRTIDIEDIRPNTLTERPRESIRIKTKTEKEKNAVYAHVLGALRSCOMLVADLYOEY 180
 QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
 DB 181 QOARDLQNRSGAMSPMNSDASTSEAS 208

Db 1 MDPLVLHSSVSSSLSELTFLKFLCIGRVGKRLKERVQSGLDLFSMLLENDLEPGHT 60
 QY 109 ELRLRLASLRHHDLRRVDDPEAGAAAGAEEDLCAAFVNICDNGKMRRLAROLK 168
 Db 61 ELRLRLASLRHHDLRRVDDPEAGAAAGAEEDLCAAFVNICDNGKMRRLAROLK 120
 QY 169 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKKNATVAHLVGLRSCOMNLVADLVQEV 228
 Db 121 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKKNATVAHLVGLRSCOMNLVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSNDSASTSEAS 256
 Db 181 QOARDLQNRSGAMSPMSNDSASTSEAS 208

RESULT 5
 AAM96154
 ID AAM96154 standard; Protein; 208 AA.
 AC AAM96154;
 XX
 DT 27-APR-1999 (first entry)
 XX
 DE Human FADD protein.
 XX
 KW FIP: FADD interacting protein; FADD: Fas-associated protein with a
 KW novel death domain; cell death; apoptosis; Alzheimer's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; muscular dystrophy;
 KW amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasma;
 KW protozoa; neoplasia; dysplasia; hyperplasia.
 XX
 OS Homo sapiens.
 PN WO9900499-A1.
 PD 07-JAN-1999.
 XX
 PF 26-JUN-1998; 98MO-US13320.
 XX
 PR 03-JUN-1998; 98US-0087886.
 PR 26-JUN-1997; 97US-0050792.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Chen TT, Williams LT;
 XX
 DR WPI; 1999-095745/08.
 DR N-PSDB; AAX08910.
 XX
 PT New FADD (Fas-associated protein with a novel death
 PT domain)-interacting Protein - useful for inducing or preventing
 PT apoptosis in a cell, to aid in controlling apoptosis-related
 PT diseases
 XX
 PS Disclosure; Page 47; 58pp; English.
 XX
 CC An epitope of human FADD (Fas-associated protein with a novel
 CC death domain)-interacting protein (FIP protein) comprising amino
 CC acids 348-727 of the protein described in AAM96153, can be used to
 CC induce or prevent apoptosis in a cell. Specifically, decreasing the
 CC levels of FIP348-727 prevents apoptosis. This is useful in cells
 CC which are dying prematurely, eg: Alzheimer's disease, Acquired
 CC Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic
 CC lateral sclerosis (and other muscle wasting diseases), autoimmune
 CC diseases, and diseases where cells are infected with a pathogen
 CC (virus, bacteria, fungus, mycoplasma or protozoa). Increasing the
 CC levels of FIP 348-727 induces apoptosis which is useful in cells
 CC suffering from neoplasias, dysplasias, hyperplasias, or their
 CC symptoms. Purified and isolated FIP subgenomic polynucleotides are
 CC useful as primers to obtain more copies of the nucleotides, and as
 CC probes that identify wild-type or mutant coding sequences. They are
 CC also useful for expressing FIP mRNA, proteins or fusion proteins,
 CC and in the generation of FIP antisense oligonucleotides and

CC ribozymes. They are also useful in expression constructs and in
 CC gene delivery vehicles (optionally in combination with a condensing
 CC agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
 CC (including variants), FIP-specific ribozymes or single-chain
 CC antibodies into eukaryotic cells. This is the human FADD protein.
 CC Human FIP protein binds to amino acids 1-110 of this sequence.
 XX
 SQ Sequence 208 AA:
 Query Match 79.9%; Score 1040; DB 20; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.7e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLHSSVSSSLSELTFLKFLCIGRVGKRLKERVQSGLDLFSMLLENDLEPGHT 108
 Db 1 MDPLVLHSSVSSSLSELTFLKFLCIGRVGKRLKERVQSGLDLFSMLLENDLEPGHT 60
 QY 109 ELRLRLASLRHHDLRRVDDPEAGAAAGAEEDLCAAFVNICDNGKMRRLAROLK 168
 Db 61 ELRLRLASLRHHDLRRVDDPEAGAAAGAEEDLCAAFVNICDNGKMRRLAROLK 120
 QY 169 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKKNATVAHLVGLRSCOMNLVADLVQEV 228
 Db 121 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKKNATVAHLVGLRSCOMNLVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSNDSASTSEAS 256
 Db 181 QOARDLQNRSGAMSPMSNDSASTSEAS 208

RESULT 6
 AAB84804
 ID AAB84804 standard; Protein; 208 AA.
 AC AAB84804;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE Human FADD prodomain.
 XX
 KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
 XX
 OS Homo sapiens.
 PN US6207458-B1.
 PD 27-MAR-2001.
 XX
 PF 07-MAY-1998; 98US-0074044.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIT) UNIT WASHINGTON.
 XX
 PI Chaudhary PM, Hood L;
 XX
 DR WPI; 2001-342087/36.
 XX
 PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
 PT activity by comparing cell activity in presence and absence of
 PT proteinaceous species having two death effector domain and test
 PT compound
 XX
 PS Disclosure; Column 51-52; 62pp; English.
 XX
 CC The present invention relates to testing candidate compounds to
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
 CC The method involves the use of 2 death effector domains (DED). The
 CC compounds identified by the invention have therapeutic
 CC applications and are useful for regulating cellular NFkappaB, JNK
 CC and apoptosis activity. The assay is useful for identifying
 CC pharmacological agents or lead compounds generally involved in
 CC assaying for compounds which regulate or modulate a cell activity.

CC The present sequence is a prodomain used in the invention.
 XX Sequence 208 AA.

Query Match 79.9%; Score 1040; DB 22; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.7e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFCIGRVYKRIKIERVQSGIDFSMLEQNDLEPGHT 108
 DB 1 MDPEVLVLSVSSSSSELTETKFCIGRVYKRIKIERVQSGIDFSMLEQNDLEPGHT 60
 QY 109 ELIRELLASIRRDLLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 168
 DB 61 ELIRELLASIRRDLLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 120
 QY 169 VSDTKIDSIDRYPRNLTERRRESLRIMKTEKENATVAHLVGLSCQNLVADLVQEV 228
 DB 121 VSDTKIDSIDRYPRNLTERRRESLRIMKTEKENATVAHLVGLSCQNLVADLVQEV 180
 QY 229 QQARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 QQARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 7
 AAB61119
 ID AAB61119 standard; protein; 208 AA.

XX AAB61119;
 XX 02-MAY-2001 (first entry)
 DE Human FADD.
 XX Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KM Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant.
 XX Homo sapiens.
 OS US6160095-A.
 PN 12-DEC-2000.
 PD 24-AUG-1999; 99US-0382155.
 PF 07-MAY-1998; 98US-0074044.
 PR (UNIT) UNIV WASHINGTON.
 PA (STOW-) STOWERS INST MEDICAL RES.
 PI Hood L, Chaudhary PM;
 DR WPL; 2001-101569/11.
 DR Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
 PT for therapeutic purposes
 XX Example 8; Fig 11; 60pp; English.
 XX The present sequence has been shown to regulate the nuclear factor-kappa
 CC B (NF-kB), Jun N-terminal kinase (JUNK), and apoptosis pathways. It
 CC is provided in a specification relating to novel mutants (D73A, L74A and
 CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
 CC and apoptosis activities. The Caspase-8 mutants are useful for
 CC therapeutic purposes and in test methods or assays for determining
 CC whether a candidate compound has a significant effect upon cell
 CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the
 CC discovery and/or design of therapeutic agents.
 XX Sequence 208 AA;
 SO

Query Match 79.3%; Score 1033; DB 22; Length 208;
 Best Local Similarity 99.0%; Pred. No. 9.1e-98;
 Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFCIGRVYKRIKIERVQSGIDFSMLEQNDLEPGHT 108
 DB 1 MDPEVLVLSVSSSSSELTETKFCIGRVYKRIKIERVQSGIDFSMLEQNDLEPGHT 60
 QY 109 ELIRELLASIRRDLLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 168
 DB 61 ELIRELLASIRRDLLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 120
 QY 169 VSDTKIDSIDRYPRNLTERRRESLRIMKTEKENATVAHLVGLSCQNLVADLVQEV 228
 DB 121 VSDTKIDSIDRYPRNLTERRRESLRIMKTEKENATVAHLVGLSCQNLVADLVQEV 180
 QY 229 QQARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 QQARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 8
 AAM87493
 ID AAM87493 standard; protein; 208 AA.

XX AAM87493;
 XX 12-FEB-1999 (first entry)

DE Amino acid sequence of MORT1 isoform MORT1G173A from human brain.

XX MORT1; MORT1d21; NTERA2; CNS; isoform; death domain; Fas/AP01;
 KM MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KM In vivo agent; neuronal apoptosis; human.

XX Homo sapiens.
 OS WO9849297-A1.
 PN 05-NOV-1998.
 PD 14-APR-1998; 98WO-US07439.
 PF 25-APR-1997; 97US-0044835.
 PR (AMHP) AMERICAN HOME PROD CORP.
 PA Birmingham BW, Birsan C, Wood AT, Young KH;
 PI WPL; 1999-009424/01.
 DR N-PSDB; AAV71930.

XX Human, neuronal MORT1 isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 XX Claim 7; Pages 30-31; 31pp; English.

XX This represents the amino acid sequence of a MORT1 isoform MORT1G173A.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209019. The cDNA has a nucleotide substitution (G
 CC to A) at basepair position 173 of the published MORT1 coding sequence.
 CC The invention relates to three MORT1 nucleic acid isoforms (AAV71928 to
 CC AAV71930) that encode proteins which can interact with the death domain
 CC of Fas/AP01. The MORT1 isoforms can also interact with MACH alpha1 or
 CC other members of the ICE/Ced3 (Caspase) family of proteins. The
 CC transcript isoforms, together with their encoded proteins are useful as
 CC screening agents in diagnosing CNS diseases, and in discovering
 CC CNS-specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.

SQ Sequence 208 AA; 79.0%; Score 1028; DB 20; Length 208;
 Query Match 98.6%; Pred. No. 3e-97;
 Best Local Similarity 98.6%; Pred. No. 3e-97;
 Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSSSSELTETKFLCGRVYKRLERVOGLDFSMLEQNDLEPGHT 108
 |||||||
 DB 1 MDPFLVLLHSVSSSSSELTETKFLCGRVYKRLERVOGLDFSMLEQNDLEPGHT 60
 |||||||
 QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFVYICDNGKMRRLAROLK 168
 |||||||
 DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFVYICDNGKMRRLAROLK 120
 |||||||
 QY 169 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
 |||||||
 DB 121 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGLRSCOMNLVADLVQEV 180
 |||||||
 QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
 |||||||
 DB 181 QOARDLQNRSGAMSPMNSDASTSEAS 208
 |||||||

RESULT 9

AAM87492
 ID AAM87492 standard; Protein; 201 AA.

AC AAM87492;
 XX
 DT 12-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of MOR1L isoform MOR1del121 from human brain.
 XX
 KM MOR1L; MOR1del121; NTERA2; CNS; Isoform; death domain; Fas/AP01;
 KM MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KM In vivo agent; neuronal apoptosis; human.
 OS Homo sapiens.
 XX
 PM W09849297-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 14-APR-1998; 98WO-US07439.
 XX
 PR 25-APR-1997; 97US-0044835.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Blingham BW, Birsan C, Wood AT, Young KH;
 PI WPI: 1999-009424/01.
 DR N-PSDB; AAV71929.
 XX
 PT Human, neuronal MOR1L isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 XX
 PS Claim 6; Pages 28-29; 31pp; English.
 XX
 CC This represents the amino acid sequence of a MOR1L isoform MOR1del121.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209018. The cDNA has a 21 base pair deletion as
 CC compared to the published MOR1L sequence (bp 172-192 of the coding
 CC sequence). The invention relates to three MOR1L nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the
 CC death domain of Fas/AP01. The MOR1L isoforms can also interact with the
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model

CC systems.
 SQ Sequence 201 AA; 75.7%; Score 985.5; DB 20; Length 201;
 Query Match 95.7%; Pred. No. 6.6e-93;
 Best Local Similarity 95.7%; Pred. No. 6.6e-93;
 Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPFLVLLHSVSSSSSELTETKFLCGRVYKRLERVOGLDFSMLEQNDLEPGHT 108
 |||||||
 DB 1 MDPFLVLLHSVSSSSSELTETKFLCGRVYKRLERVOGLDFSMLEQNDLEPGHT 57
 |||||||
 QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFVYICDNGKMRRLAROLK 168
 |||||||
 DB 58 ---ELRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFVYICDNGKMRRLAROLK 113
 |||||||
 QY 169 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
 |||||||
 DB 114 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGLRSCOMNLVADLVQEV 173
 |||||||
 QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
 |||||||
 DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201
 |||||||

RESULT 10

AAM87491
 ID AAM87491 standard; Protein; 201 AA.

AC AAM87491;
 XX
 DT 12-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of MOR1L isoform MOR1del121 from NTERA2 cells.
 XX
 KM MOR1L; MOR1del121; NTERA2; CNS; Isoform; death domain; Fas/AP01;
 KM MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KM In vivo agent; neuronal apoptosis; human.
 OS Homo sapiens.
 XX
 PM W09849297-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 14-APR-1998; 98WO-US07439.
 XX
 PR 25-APR-1997; 97US-0044835.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Blingham BW, Birsan C, Wood AT, Young KH;
 PI WPI: 1999-009424/01.
 DR N-PSDB; AAV71928.
 XX
 PT Human, neuronal MOR1L isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 XX
 PS Claim 5; Pages 26-27; 31pp; English.
 XX
 CC This represents the amino acid sequence of a MOR1L isoform MOR1del121.
 CC The encoding cDNA was isolated from NTERA2 cells and deposited under the
 CC accession number ATCC 209013. The cDNA has a 21 base pair deletion as
 CC compared to the published MOR1L sequence (bp 172-192 of the coding
 CC sequence). The invention relates to three MOR1L nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the
 CC death domain of Fas/AP01. The MOR1L isoforms can also interact with the
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy

CC either as in vivo agents in humans or as experimental tools in
CC manipulating neuronal apoptosis in cell culture and animal model
CC systems.

SO Sequence 201 AA;

Query Match 75.5%; Score 982.5; DB 20; Length 201;
Best Local Similarity 95.7%; Pred. No. 1.3e-92;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

OY 49 MDPLVILHSVSSSSSELTELKFLCIGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108

DB 1 MDPLVILHSVSSSSSELTELKFLCIGRVYKRLERVOGSLDFSMLEQNDLEPGHT 57

OY 109 ELLELLASLRHDLRRVDFEAGAAAGAPGEEDLCAPFNVICDNYGKDMRLAROLK 168

DB 58 -----ELLESLRRHDLRRVDFEAGAAAGAPGEEDLCAPFNVICDNYGKDMRLAROLK 113

OY 169 VSDTKRISIEDRYPRNLTERPRESRLRKNTKEKNAVYAHVGLRSCOMNLVADLYGEV 228

DB 114 VSDTKRISIEDRYPRNLTERPRESRLRKNTKEKNAVYAHVGLRSCOMNLVADLYGEV 173

OY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256

DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201

RESULT 11

AAB61900 standard; Protein; 205 AA.

AC AAB61900;

DT 08-MAY-2001 (first entry)

DE Mouse apoptosis mediator FADD.

KM FADD; DED; FADD-DED; death effector domain; apoptosis mediator;

KM bacterial; cell death; reactive oxygen species; ROS; mouse.

OS Mus sp.

PN MO200104153-A1.

PD 18-JAN-2001.

PF 11-JUL-2000; 2000MO-KR00721.

PR 12-JUL-1999; 99KR-0027964.

PA (IMAG-) IMAGENE CO LTD.

PI Kim S, Kim K.

DR WPI: 2001-138318/14.

DR N-PSDB: AAC85064.

PT Novel death effector domain of mammalian apoptosis mediator, for

PT inducing bacterial and mammalian cell death by enhancing cellular level

PT of reactive oxygen species -

PS Claim 1; Page 43-44; 47pp; English.

CC The invention relates to a death effector domain (DED) of a mammalian

CC apoptosis mediator (FADD). The FADD-DED induces bacterial and mammalian

CC cell death by enhancing cellular level of Reactive Oxygen Species (ROS).

CC The present sequence represents a mouse FADD, a pro-apoptotic mediator

CC consisting of N-terminal death effector domain (DED) and C-terminal death

Best Local Similarity 68.4%; Pred. No. 1.4e-65;

Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

OY 49 MDPLVILHSVSSSSSELTELKFLCIGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108

DB 1 MDPLVILHSVSSSSSELTELKFLCIGRVYKRLERVOGSLDFSMLEQNDLEPGHT 60

OY 109 ELLELLASLRHDLRRVDFEAGAAAGAPGEEDLCAPFNVICDNYGKDMRLAROLK 168

DB 61 ELLELLASLRHDLRRVDFEAGAAAGAPGEEDLCAPFNVICDNYGKDMRLAROLK 120

OY 169 VSDTKRISIEDRYPRNLTERPRESRLRKNTKEKNAVYAHVGLRSCOMNLVADLYGEV 228

DB 121 VSEAKMDIERKPPSLSERPRESRLRKNTKEKNAVYAHVGLRSCOMNLVADLYGEV 180

OY 229 QOARDLQNRSGAMSPMNSDASTSE 254

DB 181 QES--VSEKEMSPVLRDSTVSSSE 203

RESULT 12

AAB84800 standard; Protein; 83 AA.

AC AAB84800;

DT 12-JUL-2001 (first entry)

DE FADD death effector domain 1.

KM NF-kappaB; JNK; apoptosis; death effector domain; DED.

OS Homo sapiens.

PN US6207458-B1.

PD 27-MAR-2001.

PF 07-MAY-1996; 98US-0074044.

PR 07-MAY-1996; 98US-0074044.

PA (UNIT) UNIV WASHINGTON.

PI Chaudhary PM, Hood L;

DR WPI: 2001-342087/36.

PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis

PT activity by comparing cell activity in presence and absence of

PT proteinaceous species having two death effector domain and test

PT compound

PS Claim 10; Column 45-47; 62pp; English.

CC The present invention relates to testing candidate compounds to

CC determine whether they affect NF-kappaB, JNK and apoptosis activity.

CC The method involves the use of 2 death effector domains (DED). The

CC compounds identified by the invention have therapeutic

CC applications and are useful for regulating cellular NFkappaB, JNK

CC and apoptosis activity. The assay is useful for identifying

CC pharmacological agents or lead compounds generally involved in

CC assaying for compounds which regulate or modulate a cell activity.

CC The present sequence is a death effector domain of the invention.

SO Sequence 83 AA;

Query Match 30.8%; Score 401; DB 22; Length 83;
Best Local Similarity 98.8%; Pred. No. 2.2e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 49 MDPLVILHSVSSSSSELTELKFLCIGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108

DB 1 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSGLDLFSMLLEQNDLEPGHT 60
 QY 109 ELRELILASLRHDLRLRYDDE 131
 DB 61 ELRELILASLRHDLRLRYDDE 83

RESULT 13
 AAB61115
 ID AAB61115 standard; protein; 83 AA.

AC AAB61115;
 XX
 XX 02-MAY-2001 (first entry)

DE Human FADD DED1 domain.

KM Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KM Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant;
 KM death effector domain; DED.

OS Homo sapiens.

PN US6160095-A.

PD 12-DEC-2000.

PF 24-AUG-1999; 99US-0382155.

PR 07-MAY-1998; 98US-0074044.

PA (UNIM) UNIV WASHINGTON.
 PA (STOW) STOWERS INST MEDICAL RES.

PI Hood L, Chaudhary PM;

DR WPI; 2001-101569/11.

XX Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
 PT for therapeutic purposes

XX Example 8; Fig 11; 60pp; English.

XX The present sequence is a death effector domain (DED) of a protein
 CC that has been shown to regulate the nuclear factor-kappa

CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It

CC is provided in a specification relating to novel mutants (D73A, L74A and

CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK

CC and apoptosis activities. The Caspase-8 mutants are useful for

CC therapeutic purposes and in test methods or assays for determining

CC whether a candidate compound has a significant effect upon cell

CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the

CC discovery and/or design of therapeutic agents.

CC Sequence 83 AA;

QY Query Match 30.8%; Score 401; DB 22; Length 83;
 DB Best Local Similarity 98.8%; Pred. No. 2.2e-33;
 Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSGLDLFSMLLEQNDLEPGHT 108
 DB 1 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSGLDLFSMLLEQNDLEPGHT 60

QY 109 ELRELILASLRHDLRLRYDDE 131
 DB 61 ELRELILASLRHDLRLRYDDE 83

RESULT 14
 ABB81755
 ID ABB81755 standard; protein; 85 AA.

XX ABB81755;
 AC 10-SEP-2002 (first entry)
 DE Tumour necrosis factor Fas associated death domain death effector domain.

XX Tumour necrosis factor; receptor; TNFR-1; death domain; DED;

XX TNFR-1 DD; Fas associated death domain; FADD; death effector domain;

XX protein co-ordinate data.

XX Unidentified.

OS US2002045578-A1.

PN 18-APR-2002.

PF 14-MAY-2001; 2001US-0854906.

PR 22-MAY-2000; 2000US-206215P.

PA (SUKI) SUKITS S F.

PA (XUGG) XU G.

PA (LINL) LIN L.

PA (TELL) TELLIEZ J.

PA (HSU) HSU S.

PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

DR WPI; 2002-443412/47.

XX Solution comprising tumor necrosis factor receptor 1 death domain,
 PT useful for identifying potential inhibitor of tumor necrosis factor

PT receptor 1 death domain

XX Disclosure; Fig 7; 49pp; English.

XX The sequence represents the tumour necrosis Fas associated death domain
 CC death effector domain (FADD DED). The invention relates to a novel

CC solution comprising a tumour necrosis factor receptor 1 death domain. The

CC solution is useful for identifying a potential inhibitor of TNFR-1 DD,

CC for the design and selection of potent and selective inhibitors of TNF

CC signalling pathways, and for generating a three-dimensional structure for

CC an unknown molecule or molecular complex.

CC Sequence 85 AA;

QY Query Match 30.8%; Score 401; DB 23; Length 85;
 DB Best Local Similarity 98.8%; Pred. No. 2.2e-33;
 Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSGLDLFSMLLEQNDLEPGHT 108
 DB 1 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSGLDLFSMLLEQNDLEPGHT 60

QY 109 ELRELILASLRHDLRLRYDDE 131
 DB 61 ELRELILASLRHDLRLRYDDE 83

RESULT 15
 AAW76623
 ID AAW76623 standard; protein; 81 AA.

AC AAW76623;
 XX 12-JUL-1999 (first entry)

DE Human FADD protein fragment containing death effector domain.

XX Death effector domain; human; murine; anti-apoptotic; treatment;

XX HIV infection; autoimmune disease; FADD protein.

XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:35:30 ; Search time 14 Seconds
(Without alignments)
538,019 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNAPPCRFEGGILGPKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: BLOSUM62
Gapop: 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1302	100.0	256	US-08-983-502-2	Sequence 2, Appl1
2	1302	100.0	256	PCT-US95-16542-2	Sequence 2, Appl1
3	1302	100.0	256	PCT-US96-10521-2	Sequence 2, Appl1
4	1047	80.4	208	US-08-618-164-3	Sequence 3, Appl1
5	1040	79.9	208	US-09-074-044A-19	Sequence 19, Appl1
6	1033	79.3	208	US-09-382-155-19	Sequence 19, Appl1
7	1028	79.0	208	US-09-064-414-6	Sequence 6, Appl1
8	985.5	75.7	201	US-09-064-414-4	Sequence 4, Appl1
9	982.5	75.5	201	US-09-064-414-2	Sequence 2, Appl1
10	436	33.6	83	US-09-042-785A-28	Sequence 28, Appl1
11	405	31.1	84	US-08-665-220-64	Sequence 64, Appl1
12	405	31.1	84	US-09-291-692-64	Sequence 64, Appl1
13	401	30.8	83	US-09-382-155-15	Sequence 15, Appl1
14	401	30.8	83	US-09-074-044A-15	Sequence 15, Appl1
15	382	29.3	74	US-08-995-159-5	Sequence 5, Appl1
16	382	29.3	74	US-08-828-683A-25	Sequence 25, Appl1
17	318	24.4	62	US-08-894-626-5	Sequence 5, Appl1
18	318	24.4	62	US-09-187-789-48	Sequence 48, Appl1
19	128.5	9.9	250	US-09-139-600-43	Sequence 43, Appl1
20	122	9.4	180	US-09-382-155-18	Sequence 18, Appl1
21	122	9.4	180	US-09-074-044A-18	Sequence 18, Appl1
22	122	9.4	220	US-08-807-200-2	Sequence 2, Appl1
23	122	9.4	220	US-09-001-777-2	Sequence 2, Appl1
24	122	9.4	235	US-08-983-502-5	Sequence 5, Appl1
25	122	9.4	235	PCT-US96-10521-5	Sequence 5, Appl1
26	122	9.4	257	US-08-618-164-2	Sequence 2, Appl1
27	122	9.4	261	US-08-983-502-25	Sequence 25, Appl1

28	122	9.4	261	5	PCT-US96-10521-25	Sequence 25, Appl1
29	122	9.4	277	4	US-08-983-502-8	Sequence 8, Appl1
30	122	9.4	277	5	PCT-US96-10521-8	Sequence 8, Appl1
31	122	9.4	464	4	US-08-983-502-18	Sequence 18, Appl1
32	122	9.4	464	5	PCT-US96-10521-18	Sequence 18, Appl1
33	122	9.4	479	2	US-08-807-200-12	Sequence 12, Appl1
34	122	9.4	479	3	US-08-852-782-3	Sequence 3, Appl1
35	122	9.4	479	4	US-09-001-777-12	Sequence 12, Appl1
36	122	9.4	479	4	US-08-983-502-7	Sequence 7, Appl1
37	122	9.4	479	5	PCT-US96-10521-7	Sequence 7, Appl1
38	119	9.1	709	1	US-08-444-005-17	Sequence 17, Appl1
39	117	9.0	75	4	US-09-291-692-66	Sequence 66, Appl1
40	117	9.0	479	4	US-09-382-155-27	Sequence 27, Appl1
41	117	9.0	479	4	US-09-074-044A-27	Sequence 27, Appl1
42	117	9.0	479	4	US-09-074-044A-28	Sequence 28, Appl1
43	117	9.0	479	4	US-08-665-220-66	Sequence 66, Appl1
44	116	8.9	75	1	US-08-665-220-66	Sequence 66, Appl1
45	116	8.9	81	2	US-08-807-200-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-983-502-2
Sequence 2, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yuri V. GOLTSKY
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: 1linear
MOLECULE TYPE: protein
US-08-983-502-2

Query Match 100.0%; Score 1302; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNQAPECRGGGIIPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
DB 1 VNQAPECRGGGIIPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
QY 61 SLSSELTETLFLCIGRVYKRLERVOGSLDLFSMLLEQNDLEPGHTELLRELLASLR 120
DB 61 SLSSELTETLFLCIGRVYKRLERVOGSLDLFSMLLEQNDLEPGHTELLRELLASLR 120
QY 121 HOLLRVDFEAGAAAGAPGEEDCAANVTCDNVGMKRRRLARQLKVSDFKIDISLR 180
DB 121 HOLLRVDFEAGAAAGAPGEEDCAANVTCDNVGMKRRRLARQLKVSDFKIDISLR 180
QY 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCQNLVADLVOEQOARDLQNRSGA 240
DB 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCQNLVADLVOEQOARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 2

PCT-US95-16542-2

Sequence 2, Application PC/TUS9516542

GENERAL INFORMATION:

APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.

APPLICANT: WEINMURZEL, Henry

APPLICANT: WALLACH, David

APPLICANT: BOLDIN, Mark

APPLICANT: VAFIOMEYEV, Eugene

APPLICANT: METT, Igor

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL

NUMBER OF SEQUENCES: 2

TITLE OF INVENTION: RECEPTORS

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/16542

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 112022

FILING DATE: 15-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 112692

FILING DATE: 19-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114615

FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25, 618

REFERENCE/DOCKET NUMBER: WALLACH-16

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 256 amino acids

TYPE: amino acid

TOPOLOGY: 1linear

MOLECULE TYPE: protein

PCT-US95-16542-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNQAPECRGGGIIPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
DB 1 VNQAPECRGGGIIPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
QY 61 SLSSELTETLFLCIGRVYKRLERVOGSLDLFSMLLEQNDLEPGHTELLRELLASLR 120
DB 61 SLSSELTETLFLCIGRVYKRLERVOGSLDLFSMLLEQNDLEPGHTELLRELLASLR 120
QY 121 HOLLRVDFEAGAAAGAPGEEDCAANVTCDNVGMKRRRLARQLKVSDFKIDISLR 180
DB 121 HOLLRVDFEAGAAAGAPGEEDCAANVTCDNVGMKRRRLARQLKVSDFKIDISLR 180
QY 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCQNLVADLVOEQOARDLQNRSGA 240
DB 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCQNLVADLVOEQOARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 3

PCT-US96-10521-2

Sequence 2, Application PC/TUS9610521

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114, 615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114, 986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115, 319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116, 588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117, 932

FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 6,5e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNQAPRFGGGIGIPGKRDRLARASPRREGARRAGPQPRPLADPMDFVLLHSVS 60
DB 1 VNQAPRFGGGIGIPGKRDRLARASPRREGARRAGPQPRPLADPMDFVLLHSVS 60
QY 61 SLSSELTETKFLCIGRVYRKLEKRVQSGDLFSMLEQNDLPGHTELLRELLASLR 120
DB 61 SLSSELTETKFLCIGRVYRKLEKRVQSGDLFSMLEQNDLPGHTELLRELLASLR 120
QY 121 HDLLRRVDFEAGAAAGAPGEEDLCAAFNVICDNGKMRRLAROLKVSPTKIDSIEDR 180
DB 121 HDLLRRVDFEAGAAAGAPGEEDLCAAFNVICDNGKMRRLAROLKVSPTKIDSIEDR 180
QY 181 YPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEVQOARDLQNRGA 240
DB 181 YPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEVQOARDLQNRGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 4

US-08-618-164-3
Sequence 3, Application US/08618164
Patent No. 5712115

GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.

APPLICANT: Braxton, Scott Michael
APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/618.164
FILING DATE: Herewith

CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J

REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0058 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-0195

TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 791038
US-08-618-164-3

Query Match 80.4%; Score 1047; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.2e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTEKFLCIGRVYRKLEKRVQSGDLFSMLEQNDLPGHTE 108
DB 1 MDPLVLLHSVSSSSSELTEKFLCIGRVYRKLEKRVQSGDLFSMLEQNDLPGHTE 108
QY 109 ELLEELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNVICDNGKMRRLAROLK 168
DB 61 ELLEELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNVICDNGKMRRLAROLK 120
QY 169 VSDTKIDSIEDRYPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
DB 121 VSDTKIDSIEDRYPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEV 180
QY 229 QOARDLQNRGAMSPMSWNSDASTSEAS 256
DB 181 QOARDLQNRGAMSPMSWNSDASTSEAS 208

RESULT 5

US-09-074-044A-19
Sequence 19, Application US/09074044A
Patent No. 6207458

GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M

APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK- κ B, JNK AND

TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY

STATE: MISSOURI
COUNTRY: USA

ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074.044A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:

TELEPHONE: 816/474-9057
TELEFAX: 816/474-9057

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 208 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: not relevant

MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
US-09-074-044A-19

Query Match 79.9%; Score 1040; DB 4; Length 208;
Best Local Similarity 99.5%; Pred. No. 6.8e-104;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60
QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 120
QY 169 VSDTKIDISIEDRYPPNLTERRVRESLRINKTEKENATVAHLVGALRSQCNMLVADLYOEY 228
DB 121 VSDTKIDISIEDRYPPNLTERRVRESLRINKTEKENATVAHLVGALRSQCNMLVADLYOEY 180
QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208

RESULT 6

US-09-382-155-19
Sequence 19, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 19
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-19

Query Match 79.3%; Score 1033; DB 4; Length 208;
Best Local Similarity 99.0%; Pred. No. 3.9e-103;
Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60
QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 120
QY 169 VSDTKIDISIEDRYPPNLTERRVRESLRINKTEKENATVAHLVGALRSQCNMLVADLYOEY 228
DB 121 VSDTKIDISIEDRYPPNLTERRVRESLRINKTEKENATVAHLVGALRSQCNMLVADLYOEY 180
QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208

RESULT 7

US-09-064-414-6
Sequence 6, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: WOOD, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia

TITLE OF INVENTION: Neuronal MOR1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-064-414-6

Query Match 79.0%; Score 1028; DB 4; Length 208;
Best Local Similarity 98.6%; Pred. No. 1.3e-102;
Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60
QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 120
QY 169 VSDTKIDISIEDRYPPNLTERRVRESLRINKTEKENATVAHLVGALRSQCNMLVADLYOEY 228
DB 121 VSDTKIDISIEDRYPPNLTERRVRESLRINKTEKENATVAHLVGALRSQCNMLVADLYOEY 180
QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208

RESULT 8

US-09-064-414-4
Sequence 4, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: WOOD, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia
TITLE OF INVENTION: Neuronal MOR1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-4

Query Match 75.7%; Score 985.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 4.7e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPELVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPHT 108
DB 1 MDPELVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPHT 57
QY 109 ELRLSLRRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRRLAROLK 168
DB 58 ----ELASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRRLAROLK 113
QY 169 VSDTKRIDSIEDRYPNLTERVRESLRINKTEKENATVAHLVGAALRSCOMNLVADLVQEV 228
DB 114 VSDTKRIDSIEDRYPNLTERVRESLRINKTEKENATVAHLVGAALRSCOMNLVADLVQEV 173
QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201

RESULT 9
US-09-064-414-2
Sequence 2, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Bitson, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany,
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.

REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-2

Query Match 75.5%; Score 982.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 9.8e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPELVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPHT 108
DB 1 MDPELVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPHT 57
QY 109 ELRLSLRRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRRLAROLK 168
DB 58 ----ELASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDMRRRLAROLK 113
QY 169 VSDTKRIDSIEDRYPNLTERVRESLRINKTEKENATVAHLVGAALRSCOMNLVADLVQEV 228
DB 114 VSDTKRIDSIEDRYPNLTERVRESLRINKTEKENATVAHLVGAALRSCOMNLVADLVQEV 173
QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201

RESULT 10
US-09-042-785A-28
Sequence 28, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-28

Query Match 33.6%; Score 438; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 9.1e-40;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LCAAFNYICDVGWDMRLAQLQVSPDKISIDRYRNTERTYRESLRITWKTENKA 204
DB 1 LCAAFNYICDVGWDMRLAQLQVSPDKISIDRYRNTERTYRESLRITWKTENKA 60
QY 205 TVALHVGALRSCQNMVLADVOEQV 229
DB 61 TVALHVGALRSCQNMVLADVOEQV 85

RESULT 11
US-08-665-220-64
Sequence 64, Application US/08665220
Patent No. 5786173

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,220
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/618,408
FILING DATE: 19-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2165.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "human FADD"

US-08-665-220-64

Query Match 31.1%; Score 405; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 3.2e-36;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVYLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPLVYLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108

DB 1 MDPLVYLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60
QY 109 ELRELALSLRRHDLRRVDDFEA 132
DB 61 ELRELALSLRRHDLRRVDDFEA 84

RESULT 12
US-09-291-692-64
Sequence 64, Application US/09291692
Patent No. 6287795

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,692
FILING DATE: 04-13-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christensen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "human FADD"

US-09-291-692-64

Query Match 31.1%; Score 405; DB 4; Length 84;
Best Local Similarity 98.8%; Pred. No. 3.2e-36;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVYLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPLVYLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
QY 109 ELRELALSLRRHDLRRVDDFEA 132
DB 61 ELRELALSLRRHDLRRVDDFEA 84

RESULT 13
US-09-382-155-15
Sequence 15, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 15
LENGTH: 83
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-15

Query Match 30.8%; Score 401; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 8.3e-36;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTETKLCIGRYVKRLRVSGDLFSMLLEQNDLEPGHT 108
DB 1 MDPLVLLHSVSSSSSELTETKLCIGRYVKRLRVSGDLFSMLLEQNDLEPGHT 60
QY 109 ELRELLASLRHDLRRVDDE 131
DB 61 ELRELLASLRHDLRRVDDE 83

RESULT 14
US-09-074-044A-15

Sequence 15, Application US/09074044A
Patent No. 6207458
GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M

APPLICANT: HOOD, LEROY

TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400

CITY: KANSAS CITY

STATE: MISSOURI

COUNTRY: USA

ZIP: 64108

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074,044A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COLLINS, JOHN M

REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 26588

TELECOMMUNICATION INFORMATION:

TELEPHONE: 816/474-9050

TELEFAX: 816/474-9057

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 83 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: not relevant

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-074-044A-15

Query Match 30.8%; Score 401; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 8.3e-36;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTETKLCIGRYVKRLRVSGDLFSMLLEQNDLEPGHT 108
DB 1 MDPLVLLHSVSSSSSELTETKLCIGRYVKRLRVSGDLFSMLLEQNDLEPGHT 60
QY 109 ELRELLASLRHDLRRVDDE 131
DB 61 ELRELLASLRHDLRRVDDE 83

RESULT 15
US-08-995-159-5

Sequence 5, Application US/08995159

Patent No. 6130079

GENERAL INFORMATION:

APPLICANT: DIXIT, VISHVA M.

APPLICANT: NI, JIAN

TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/995,159

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/033,868

FILING DATE: 20-DEC-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: GOLDSTEIN, JORGE A.

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 1488,0860001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 74 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-995-159-5

Query Match 29.3%; Score 382; DB 4; Length 74;

Best Local Similarity 100.0%; Pred. No. 7.8e-34;

Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNKGKDWRLAROLKYSDFIKDISIEDRYPRNLTERRYRESLRINKTEKENATVAHLVG 211
DB 1 ICDNKGKDWRLAROLKYSDFIKDISIEDRYPRNLTERRYRESLRINKTEKENATVAHLVG 60

QY 212 ALRSCOMLVADLV 225
DB 61 ALRSCOMLVADLV 74

Thu Jun 19 11:26:31 2003

Search completed: June 19, 2003, 10:39:27
Job time : 15 secs

us-09-933-814-2_1.ra1

Page 8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:38:50 ; Search time 48 Seconds
(without alignments)
577.103 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNQAPRCFRGGILGPIGRK.....RSGAMSPMSNNSDASTSEAS 256

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US08_NMW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NMW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NMW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NMW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NMW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1302	100.0	256	10 US-09-933-814-2	Sequence 2, Appl
2	1302	100.0	256	10 US-09-824-134-2	Sequence 2, Appl
3	405	31.1	84	10 US-09-952-768-64	Sequence 64, Appl
4	390	30.0	81	10 US-09-410-194-9	Sequence 9, Appl
5	386	29.6	82	9 US-10-001-254-39	Sequence 39, Appl
6	382	29.3	74	9 US-10-112-793-25	Sequence 25, Appl
7	382	29.3	74	9 US-10-287-594-5	Sequence 5, Appl
8	369	28.3	77	9 US-10-001-234-35	Sequence 35, Appl
9	318	24.4	62	12 US-10-035-408-5	Sequence 5, Appl
10	128.5	9.9	250	10 US-10-068-564-48	Sequence 48, Appl
11	128.5	9.9	250	10 US-09-989-903-48	Sequence 48, Appl
12	122	9.4	177	10 US-09-410-194-7	Sequence 7, Appl
13	122	9.4	478	9 US-09-009-893-3	Sequence 3, Appl
14	122	9.4	479	10 US-09-410-194-20	Sequence 20, Appl
15	117	9.0	75	10 US-09-952-768-66	Sequence 66, Appl
16	116	8.9	75	9 US-10-001-234-31	Sequence 31, Appl
17	116	8.9	110	10 US-09-864-761-36543	Sequence 36543, A
18	116	8.9	476	10 US-09-954-697-27	Sequence 27, Appl
19	116	8.9	496	10 US-09-952-768-4	Sequence 4, Appl

20	115.5	8.9	656	10 US-09-862-027-30	Sequence 30, Appl
21	111.5	8.6	77	9 US-10-287-594-7	Sequence 7, Appl
22	111.5	8.6	671	9 US-09-981-357A-16	Sequence 16, Appl
23	111.5	8.6	671	10 US-09-758-003-2	Sequence 2, Appl
24	111.5	8.6	671	10 US-09-862-027-29	Sequence 29, Appl
25	110	8.4	221	10 US-09-410-194-15	Sequence 15, Appl
26	110	8.4	221	10 US-09-410-194-22	Sequence 22, Appl
27	110	8.4	480	9 US-09-009-893-2	Sequence 2, Appl
28	110	8.4	480	10 US-09-861-270-2	Sequence 2, Appl
29	110	8.4	480	10 US-09-410-194-11	Sequence 11, Appl
30	110	8.4	480	10 US-09-410-194-17	Sequence 17, Appl
31	108.5	8.3	77	9 US-10-112-793-27	Sequence 27, Appl
32	108	8.3	79	10 US-09-952-768-65	Sequence 65, Appl
33	108	8.3	170	10 US-09-410-194-8	Sequence 8, Appl
34	108	8.3	479	9 US-09-009-893-3	Sequence 4, Appl
35	108	8.3	479	10 US-09-952-768-2	Sequence 2, Appl
36	108	8.3	479	10 US-09-954-697-33	Sequence 33, Appl
37	108	8.3	521	10 US-09-962-834A-2	Sequence 2, Appl
38	108	8.3	571	10 US-09-410-194-21	Sequence 21, Appl
39	106	8.1	77	9 US-10-001-254-33	Sequence 33, Appl
40	92.5	7.1	909	9 US-09-925-299-988	Sequence 988, App
41	92.5	7.1	909	10 US-09-925-299-988	Sequence 988, App
42	92.5	7.1	298	10 US-09-801-368-230	Sequence 230, App
43	91.5	7.0	832	10 US-09-834-765-2	Sequence 2, Appl
44	91	7.0	2743	9 US-10-037-187-36	Sequence 36, Appl
45	91	7.0	3695	9 US-10-037-182-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1	US-09-933-814-2	Sequence 2, Application US/09933814
Patent No.	US20020058798A1	
GENERAL INFORMATION:		
APPLICANT:	WALLACH, David	
APPLICANT:	BOLDIN, Mark	
APPLICANT:	VARFOLOMEY, Eugene	
TITLE OF INVENTION:	MODULATORS OF THE FUNCTION OF FAS/ABOI RECEPTORS	
FILE REFERENCE:	WALLACH-16B	
CURRENT APPLICATION NUMBER:	US/09/933, 814	
CURRENT FILING DATE:	2001-08-22	
PRIOR APPLICATION NUMBER:	08/860, 082	
PRIOR FILING DATE:	1997-08-19	
PRIOR APPLICATION NUMBER:	PCT/US95/16542	
PRIOR FILING DATE:	1995-12-14	
PRIOR APPLICATION NUMBER:	IL 112022	
PRIOR FILING DATE:	1994-12-15	
PRIOR APPLICATION NUMBER:	IL 112692	
PRIOR FILING DATE:	1995-02-19	
NUMBER OF SEQ ID NOS:	2	
SOFTWARE:	Patentin version 3.0	
SEQ ID NO 2		
LENGTH:	256	
TYPE:	PRT	
ORGANISM:	Homo sapiens	
US-09-933-814-2		
Query Match	100.0%	Score 1302; DB 10; Length 256;
Best Local Similarity	100.0%	Pred. No. 2.8e-113;
Matches	256; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 VNQAPRCFRGGILGPIGRKRDLASAEPRTGARRAGQPPPLADPMDPLVLLHSVS 60	Sequence 30, Appl
DB	1 VNQAPRCFRGGILGPIGRKRDLASAEPRTGARRAGQPPPLADPMDPLVLLHSVS 60	Sequence 16, Appl
QY	61 SLSSESETEKFLCIGRVYKRLRVSQGLDFSMLEQNDLEFGHTELLRELLASLR 120	Sequence 2, Appl
DB	61 SLSSESETEKFLCIGRVYKRLRVSQGLDFSMLEQNDLEFGHTELLRELLASLR 120	Sequence 29, Appl
QY	121 HDLARVDPEFGAAGAGAEDELCAPFNVICDVGQWRLANQIAVSDIKIDSIEDR 180	Sequence 15, Appl
DB	121 HDLARVDPEFGAAGAGAEDELCAPFNVICDVGQWRLANQIAVSDIKIDSIEDR 180	Sequence 22, Appl

Db 121 HDLLRRVDEEAGAAAGAEEDLCAAFNYICDVGKDWRRRLARQLKVSPTKIDSIEDR 180
QY 181 YPRNLTERVRESLIRKMTKEKNATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
Db 181 YPRNLTERVRESLIRKMTKEKNATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
QY 241 MSPMSNSDASTSEAS 256
Db 241 MSPMSNSDASTSEAS 256

RESULT 2

US-09-824-134-2

Sequence 2, Application US/09824134

Patent No. US20020082401A1

GENERAL INFORMATION:

APPLICANT: WALLACH, David

BOLDIN, Mark

VARFOLOMEY, Eugene

METT, Igor

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824.134

FILING DATE: 03-Apr-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/860,082

FILING DATE: <Unknown>

APPLICATION NUMBER: IL 112022

FILING DATE: 15-DEC-1994

APPLICATION NUMBER: IL 112692

FILING DATE: 19-FEB-1995

APPLICATION NUMBER: IL 114615

FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25, 618

REFERENCE/DOCKET NUMBER: WALLACH-16

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 256 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-824-134-2

Query Match 100.0%; Score 1302; DB 10; Length 256;

Best Local Similarity 100.0%; Pred. NO. 2.8e-113; Indels 0; Gaps 0;

Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAECFFGGGIIIGPLGKRRDLAAASEPRTEGARAGPOPPPLADPAMPDFLVLLHSYS 60

Db 1 VNOAECFFGGGIIIGPLGKRRDLAAASEPRTEGARAGPOPPPLADPAMPDFLVLLHSYS 60

QY 61 SSLSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHTELLRELLASLRR 120

Db 61 SSLSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHTELLRELLASLRR 120
QY 121 HDLLRRVDEEAGAAAGAEEDLCAAFNYICDVGKDWRRRLARQLKVSPTKIDSIEDR 180
Db 121 HDLLRRVDEEAGAAAGAEEDLCAAFNYICDVGKDWRRRLARQLKVSPTKIDSIEDR 180
QY 181 YPRNLTERVRESLIRKMTKEKNATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
Db 181 YPRNLTERVRESLIRKMTKEKNATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
QY 241 MSPMSNSDASTSEAS 256
Db 241 MSPMSNSDASTSEAS 256

RESULT 3

US-09-952-768-64

Sequence 64, Application US/09952768

Patent No. US20020035242A1

GENERAL INFORMATION:

APPLICANT: Alnemrl, Enad S.

Fernandes-Alnemrl, Teresa

Litwack, Gerald

Armstrong, Robert

Tomasselli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,

NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: Suite 6300, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christensen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..84

OTHER INFORMATION: /note="human FADD"

SEQUENCE DESCRIPTION: SEQ ID NO: 64:

US-09-952-768-64

Query Match 31.1%; Score 405; DB 10; Length 84;

Best Local Similarity 98.8%; Pred. NO. 1.8e-30; Indels 0; Gaps 0;

Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108

Db 1 MDPLVLLHSVSSSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60

QY 109 ELRELLASLRHDLRRVDDEFA 132
DB 61 ELRELLASLRHDLRRVDDEFA 84

RESULT 4

US-09-410-194-9
Sequence 9, Application US/09410194
Patent No. US20020095030A1

GENERAL INFORMATION:

APPLICANT: Tschopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Irmeler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean- Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay

APPLICANT: French, E. Lairs

TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS

FILE REFERENCE: 11141-002001

CURRENT APPLICATION NUMBER: US/09/410,194

CURRENT FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: PCT/EP98/01857

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 81

TYPE: PRT

ORGANISM: Homo sapiens

US-09-410-194-9

Query Match 30.0%; Score 390; DB 10; Length 81;
Best Local Similarity 96.8%; Pred. No. 4.2e-29;
Matches 80; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLHSSVSSLSSELTETKFLGIRYVKRLERVOGGLDFSLLEQNDLEPGHT 108
DB 1 MDPLVLHSSVSSLSSELTETKFLGIRYVKRLERVOGGLDFSLLEQNDLEPGHT 60

QY 109 ELRELLASLRHDLRRVD 129
DB 61 ELRELLASLRHDLRRVD 81

RESULT 5

US-10-001-254-39
Sequence 39, Application US/10001254
Publication No. US20030049702A1

GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Stenner-llewen, Frank
TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 39
LENGTH: 82
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-254-39

Query Match 29.6%; Score 386; DB 9; Length 82;
Best Local Similarity 96.4%; Pred. No. 1e-28;
Matches 80; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 49 MDPLVLHSSVSSLSSELTETKFLGIRYVKRLERVOGGLDFSLLEQNDLEPGHT 108
DB 1 MDPLVLHSSVSSLSSELTETKFLGIRYVKRLERVOGGLDFSLLEQNDLEPGHT 58

QY 109 ELRELLASLRHDLRRVDDE 131
DB 59 ELRELLASLRHDLRRVDDE 81

RESULT 6

US-10-112-793-25
Sequence 25, Application US/10112793
Publication No. US20020192739A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,793

FILING DATE: 28-Mar-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marshchang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P100761

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 74 amino acids

TYPE: AMINO ACID

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-10-112-793-25

Query Match 29.3%; Score 382; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDVNGKMRRLARQLKYSIDKIDSIERYRPNLTERVRESLRIRKTKENATVAHLVG 211
DB 1 ICDVNGKMRRLARQLKYSIDKIDSIERYRPNLTERVRESLRIRKTKENATVAHLVG 60

Oy 212 ALRSCOMNLVADLV 225
Db 61 ALRSCOMNLVADLV 74

RESULT 7

US-10-287-594-5
Sequence 5, Application US/10287594
Publication No. US20030096288A1
GENERAL INFORMATION:
APPLICANT: Nt, Jlan
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: RAIDD, A NO. US20030096288A1el Death Adaptor Molecule
FILE REFERENCE: 1488, 0860002
CURRENT FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US/09/545,605
PRIOR FILING DATE: 2001-04-07
PRIOR APPLICATION NUMBER: 08/995,159
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60,033,868
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-594-5

Query Match 29.3%; Score 382; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 2, 1e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 152 ICDNVGKDMRLAROLKVSDEKIDRIEDRYPRNLTERRVRESLRITWKTEKENATVAHLVG 211
Db 1 ICDNVGDMRLAROLKVSDEKIDRIEDRYPRNLTERRVRESLRITWKTEKENATVAHLVG 60

Oy 212 ALRSCOMNLVADLV 225
Db 61 ALRSCOMNLVADLV 74

RESULT 8

US-10-001-254-35
Sequence 35, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Florentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfried
APPLICANT: Stenner-Ilewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-254-35

Query Match 28.3%; Score 369; DB 9; Length 77;
Best Local Similarity 98.7%; Pred. No. 3, 6e-27;

Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 49 MDPELVILHSVSSLSSELTETKFLCIGRVKRLERVOSGIDLFSMLLEQNDLEPGHT 108
Db 1 MDPELVILHSVSSLSSELTETKFLCIGRVKRLERVOSGIDLFSMLLEQNDLEPGHT 60

Oy 109 ELRELLASLRHDLR 125
Db 61 ELRELLASLRHDLR 77

RESULT 9

US-10-035-408-5
Sequence 5, Application US/10035408
Patent No. US20020123117A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark P.
VARPOLOMEY, Eugene E.
PANCER, Zeev
METZ, Igor
GONCHAROV, Tanya M.
WEINMURZEL, Henry
TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/035,408
FILING DATE: 04-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 737-3528
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-035-408-5

Query Match 24.4%; Score 318; DB 12; Length 62;
Best Local Similarity 100.0%; Pred. No. 1, 5e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 160 WRRLAROLKVSDEKIDRIEDRYPRNLTERRVRESLRITWKTEKENATVAHLVGALRSCOMN 219
Db 1 WRRLAROLKVSDEKIDRIEDRYPRNLTERRVRESLRITWKTEKENATVAHLVGALRSCOMN 60

OY 220 LV 221
DB 61 LV 62

RESULT 10

US-10-068-564-48
Sequence 48, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068, 564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 48
LENGTH: 250
TYPE: PRT
ORGANISM: Mus musculus
US-10-068-564-48

Query Match 9.9%; Score 128.5; DB 9; Length 250;
Best Local Similarity 40.8%; Pred. No. 0.0004; Indels 1; Gaps 1;
Matches 31; Conservative 12; Mismatches 32;

OY 49 MDPLVLHVSYSLSSELTFLKLCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MD-PQSLDIAAEELGSEDLAALKFLCLDYPHKKLTIERACKFLRLRKGMLEBGNL 59
OY 109 ELRELLASLRHDL 124
DB 60 SFLELLFHSRMDL 75

US-09-989-903-48
Sequence 48, Application US/09989903
Patent No. US20020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434D1
CURRENT APPLICATION NUMBER: US/09/989, 903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 48
LENGTH: 250
TYPE: PRT
ORGANISM: Mus musculus
US-09-989-903-48

Query Match 9.9%; Score 128.5; DB 9; Length 250;
Best Local Similarity 40.8%; Pred. No. 0.0004; Indels 1; Gaps 1;
Matches 31; Conservative 12; Mismatches 32;

OY 49 MDPLVLHVSYSLSSELTFLKLCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MD-PQSLDIAAEELGSEDLAALKFLCLDYPHKKLTIERACKFLRLRKGMLEBGNL 59
OY 109 ELRELLASLRHDL 124
DB 60 SFLELLFHSRMDL 75

US-09-989-903-48
Sequence 48, Application US/09989903
Patent No. US20020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434D1
CURRENT APPLICATION NUMBER: US/09/989, 903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 48
LENGTH: 250
TYPE: PRT
ORGANISM: Mus musculus
US-09-989-903-48

Query Match 9.9%; Score 128.5; DB 10; Length 250;
Best Local Similarity 40.8%; Pred. No. 0.0004; Indels 1; Gaps 1;
Matches 31; Conservative 12; Mismatches 32;

OY 49 MDPLVLHVSYSLSSELTFLKLCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MD-PQSLDIAAEELGSEDLAALKFLCLDYPHKKLTIERACKFLRLRKGMLEBGNL 59
OY 109 ELRELLASLRHDL 124
DB 60 SFLELLFHSRMDL 75

US-09-989-903-48
Sequence 48, Application US/09989903
Patent No. US20020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434D1
CURRENT APPLICATION NUMBER: US/09/989, 903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 48
LENGTH: 250
TYPE: PRT
ORGANISM: Mus musculus
US-09-989-903-48

Query Match 9.9%; Score 128.5; DB 10; Length 250;
Best Local Similarity 40.8%; Pred. No. 0.0004; Indels 1; Gaps 1;
Matches 31; Conservative 12; Mismatches 32;

OY 49 MDPLVLHVSYSLSSELTFLKLCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MD-PQSLDIAAEELGSEDLAALKFLCLDYPHKKLTIERACKFLRLRKGMLEBGNL 59
OY 109 ELRELLASLRHDL 124
DB 60 SFLELLFHSRMDL 75

RESULT 12

US-09-410-194-7
Sequence 7, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Tschopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Imbler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lais
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410, 194
CURRENT FILING DATE: 1999-09-30
PRIORITY APPLICATION NUMBER: PCT/EP98/01857
PRIORITY FILING DATE: 1998-03-31
PRIORITY APPLICATION NUMBER: GERMANY 197 13 393.2
PRIORITY FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 7
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-7

Query Match 9.4%; Score 122; DB 10; Length 177;
Best Local Similarity 28.8%; Pred. No. 0.001; Indels 16; Gaps 4;
Matches 38; Conservative 23; Mismatches 55;

OY 56 LHSVSSLSSELTFLKLCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 115
DB 7 LYDIGEQLSDSDIASIKFLSDYIPORQEPRIKXALMFQRLQEKRLMEENSLKRL 66
OY 116 ASLRHDL-----RRVDFEAGAAAGAPGEDICAAFNVCNDVGMRR-----L 163
DB 67 FRINRLDLITYLWTRKEMEREL--QTPGRACI-SAYRYWLYQISSEVSRSLSRPF 122
OY 164 ARLKVSPTKID 175
DB 123 LLOEISCKRID 134

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-009-893-3
Sequence 3, Application US/09008993
Publication No. US2003008739A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-3

Query Match
Best Local Similarity 28.8%; Score 122; DB 9; Length 478;
Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

QY 56 LHSVSSLSSELTETKFLCIGRVKRLERVOGSLDLSMLLEQNDLPGHTELLRELL 115
DB 7 LVDIGQDSEDLASKFLSLDYIPQRKQEPIDALMFORLQEKMLESNLSFLKELL 66
QY 116 ASLRHDL-----RVDDFEGAAGAAGPEEDLCAAFNYICDNYGKMRR-----L 163
DB 67 FRNRDLITYINTRKEMEREL---QTPGRAQI-SAYRVMLYQISEEVSSELSRFR 122
QY 164 ANQLKVSDFKID 175
DB 123 LQEEISKCKLD 134

RESULT 14
US-09-410-194-20
Sequence 20, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Techopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Imtler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Iars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 1141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 479

TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-20

Query Match
Best Local Similarity 28.8%; Score 122; DB 10; Length 479;
Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

QY 56 LHSVSSLSSELTETKFLCIGRVKRLERVOGSLDLSMLLEQNDLPGHTELLRELL 115
DB 7 LVDIGQDSEDLASKFLSLDYIPQRKQEPIDALMFORLQEKMLESNLSFLKELL 66
QY 116 ASLRHDL-----RVDDFEGAAGAAGPEEDLCAAFNYICDNYGKMRR-----L 163
DB 67 FRNRDLITYINTRKEMEREL---QTPGRAQI-SAYRVMLYQISEEVSSELSRFR 122
QY 164 ANQLKVSDFKID 175
DB 123 LQEEISKCKLD 134

RESULT 15
US-09-952-768-66
Sequence 66, Application US/09952768
Patent No. US20020035242A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140,424C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
FEATURE:
NAME/KEY: peptide
LOCATION: 1-75
OTHER INFORMATION: /note- "Mch5 A"
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-952-768-66

Query Match
Best Local Similarity 39.1%; Score 117; DB 10; Length 75;
Matches 27; Conservative 11; Mismatches 31; Indels 0; Gaps 0;

QY 56 LHSVSSLSSELTELKFCIGRVKRLERVOGJDLFSLLEONDLPEGHTELLREL 115
 Db 4 LVDIGEOJDEBDLASLFLSLDPTIPQRKQEPKDALMLFQRLQEKRLLESNLSFLKELL 63

QY 116 ASLRHDL 124
 Db 64 FRIRHDL 72

Search completed: June 19, 2003, 10:44:49
 Job time : 49 secs

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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:35:05 ; Search time 18 Seconds
(without alignments)
1367.245 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VQNAPECRGCGGILGPKR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	79.9	208	2 A56912	FADD protein - hum
2	121.5	9.3	1856	2 B35049	ankyrin 1, erythro
3	121.5	9.3	1880	2 A35049	ankyrin 1, erythro
4	121.5	9.3	1881	1 SJHUK	ankyrin 1, erythro
5	117.5	9.0	1848	2 S37771	ankyrin, erythrocy
6	117.5	9.0	1862	2 I49502	ankyrin - mouse
7	115.5	8.9	655	2 I49289	receptor interacti
8	111.5	8.6	671	2 T09479	serine/threonine p
9	103	7.9	2039	2 T15347	ankyrin-related un
10	99	7.6	1955	2 F83257	hypothetical prote
11	99	7.6	1955	2 T30934	myosin-like protei
12	99	7.6	3924	2 S37431	ankyrin 2, neurona
13	98.5	7.6	4644	1 A38905	dynein heavy chain
14	97	7.5	622	2 A84290	glu-tRNA amidotran
15	96.5	7.4	1162	2 T49191	hypothetical prote
16	96	7.4	647	2 F83087	probable chemotaxi
17	95.5	7.3	497	2 F83087	RNA polymerase sig
18	95.5	7.3	509	2 H87685	conserved hypotet
19	95	7.3	406	2 G70639	hypothetical prote
20	95	7.3	414	2 T35625	probable sensor-11
21	94.5	7.3	497	2 A53373	ribosome receptor,
22	94	7.2	1534	2 A56734	iron protein - pse
23	93.5	7.2	324	2 JC2395	Fas antigen precur
24	91.5	7.0	470	2 F70621	probable arch prot
25	91.5	7.0	763	2 A82863	hypothetical prote
26	91	7.0	809	2 G75605	hypothetical prote
27	91	7.0	1029	2 H96658	hypothetical prote
28	90.5	7.0	130	2 S55385	PA-15 protein - m
29	90.5	7.0	411	2 S45318	keratin 12 - rabbi

30	90.5	7.0	2427	2 T16613	hypothetical prote
31	90	6.9	520	2 S35575	myosin heavy chain
32	90	6.9	725	2 A47168	cardiac morphogene
33	89.5	6.9	536	1 A47190	transducer protein
34	89.5	6.9	536	2 E84318	Hrt1 transducer (1
35	89.5	6.9	1816	1 S68960	laminin alpha-4 ch
36	89	6.8	483	2 A55033	keratin 12 - mouse
37	88.5	6.8	130	2 S55384	PA-15 protein - h
38	88.5	6.8	807	2 T00980	hypothetical prote
39	88.5	6.8	892	1 FADDA	alpha actinin 1 -
40	88.5	6.8	1927	2 A59236	embryonic muscle m
41	87.5	6.7	294	2 A11617	protein secretion
42	87.5	6.7	433	2 A32992	cyclin B1 - human
43	87.5	6.7	1732	2 G84664	hypothetical prote
44	87.5	6.7	3433	2 S28381	utrophin - human
45	87.5	6.7	4377	2 A55375	ankyrin 3, long sp

ALIGNMENTS

RESULT 1

A56912

FADD protein - human

N:Alternate names: FAS-associating death domain containing protein FADD; mediator of

C:Species: Homo sapiens (man)

C>Date: 11-Aug-1995 #sequence, revision 11-Aug-1995 #text, change 01-Dec-2000

C:Accession: A56912; I38041

R:Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.

Cell 81, 505-512, 1995

A>Title: FADD, a novel death domain-containing protein, interacts with the death doma

A:Reference number: A56912; MUID:95277837; PMID:7538907

A:Accession: A56912

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <CHI>

A:Cross-references: GB:U24231; NID:9809486; PID:AAA8517.1; PID:9809487

R:Boldin, M.P.; Varfolomeev, E.E.; Pancar, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D.

J. Biol. Chem. 270, 7793-7798, 1995

A>Title: A novel protein that interacts with the death domain of Fas/Abol contains a

A:Reference number: I38041; MUID:95229578; PMID:7536190

A:Accession: I38041

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-31, V, 33-208 <RES>

A:Cross-references: EMBL:X84709; NID:9791037; PID:CAA59197.1; PID:9791038

C:Genetics:

A:Gene: GDB:FADD; MORT1

A:Cross-references: GDB:1320394

C:Superfamily: receptor-induced toxicity mediator MORT1

C:Keywords: apoptosis

Query Match 79.9%; Score 1040; DB 2; Length 208;

Best Local Similarity 99.5%; Pred. No. 2.3e-75;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	49	MDPFLVILHSVSSLSSELTETKFLCGRVYKRLERVOGDLFSLLEQNDLEPHT	108
DB	1	MDPFLVILHSVSSLSSELTETKFLCGRVYKRLERVOGDLFSLLEQNDLEPHT	60
QY	109	ELRELASLRRLRLRRVDDEFGAAGAAPGEDCAAFNVICDNVGRRLAROLK	168
DB	61	ELRELASLRRLRLRRVDDEFGAAGAAPGEDCAAFNVICDNVGRRLAROLK	120
QY	169	VSDTKIDSIEDRYRNLTERRVRESLRITKNTKRNATVAHLVGLRSCQNLVADLVQEV	228
DB	121	VSDTKIDSIEDRYRNLTERRVRESLRITKNTKRNATVAHLVGLRSCQNLVADLVQEV	180
QY	229	QOARDLNRSGAMSPMSWNSDASTSEAS	256
DB	181	QOARDLNRSGAMSPMSWNSDASTSEAS	208

RESULT 2
B35049
ankyrin 1, erythrocyte splice form 3 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C:Accession: B35049
R:Lambert, S.; Yu, H.; Pichal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370; PMID:1689849
A:Accession: B35049
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1856 <AM>
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin repeat homology
C:Keywords: alternative splicing
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <AM>
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
Query Match 9.3%; Score 121.5; DB 2; Length 1856;
Best Local Similarity 27.2%; Pred. No. 0.3;
Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;
OY 137 GAAGEEDLCFAFVNDVNGKRRRLAKVSDTKSDIEDRPRRLTRVRESLRIM 196
DB 1395 GSLGTFQAEKMAVISEHLQSWAELEKLEQFVEDINRIRVENPNSLQSVALLNIM 1454
OY 197 KTEKENATVAHLVGLARSCOMNLVADLVQ-EVQOARDLQ-----NNSGAMSPMSNSD 249
DB 1455 VIRGQNNMNTLTALQSIDRGEIVNMLESGSGRSRLKRPDRHTDQYLSLSPSONNGY 1514
OY 250 ASTSE 254
DB 1515 SSLAD 1519
RESULT 3
A35049
ankyrin 1, erythrocyte splice form 2 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)
C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
C:Accession: A35049

R:Lambert, S.; Yu, H.; Pichal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370; PMID:1689849
A:Accession: A35049
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1880 <AM>
A:Cross-references: GB:M28880
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin repeat homology
C:Keywords: alternative splicing; cytoskeleton
F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <AM>
F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
Query Match 9.3%; Score 121.5; DB 2; Length 1880;
Best Local Similarity 27.2%; Pred. No. 0.3;
Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;
OY 137 GAAGEEDLCFAFVNDVNGKRRRLAKVSDTKSDIEDRPRRLTRVRESLRIM 196
DB 1395 GSLGTFQAEKMAVISEHLQSWAELEKLEQFVEDINRIRVENPNSLQSVALLNIM 1454
OY 197 KTEKENATVAHLVGLARSCOMNLVADLVQ-EVQOARDLQ-----NNSGAMSPMSNSD 249
DB 1455 VIRGQNNMNTLTALQSIDRGEIVNMLESGSGRSRLKRPDRHTDQYLSLSPSONNGY 1514
OY 250 ASTSE 254
DB 1515 SSLAD 1519
RESULT 4
S3HUR
ankyrin 1, erythrocyte splice form 1 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S08275; A33219; PC2220; A35443
R:Liux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A:Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
A:Reference number: S08275; MUID:90158830; PMID:2137537
A:Accession: S08275
A:Molecule type: mRNA
A:Residues: 1-1881 <L01>

A:Cross-references: EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
 A:Accession: A33219
 A:Molecule type: Protein
 A:Residues: 217, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X',
 X, 1367, 1383-1427, 1601-1630, 1686-1698, 'D', 1700, 1763-1772 <LUX>
 A:Note: 845-Ary and 1392-Thr were also found
 R.Hermann, J.; Barel, M.; Frade, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994
 A:Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
 A:Reference number: PC2220; MUID:95077348; PMID:7526850
 A:Accession: PC2220
 A:Molecule type: protein
 A:Residues: 910-929 <HER>
 R.Davis, L.H.; Bennett, V.
 J. Biol. Chem. 265, 10589-10596, 1990
 A:Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
 A:Reference number: A35443; MUID:90285190; PMID:2141335
 A:Accession: A35443
 A:Molecule type: protein
 A:Residues: 'X', 5, 'X', 7-12, 403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814, 862-863,
 C:Genetics:
 A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing; phosphoprotein
 F:2-1881/Product: ankyrin 1, erythrocyte form 1 status predicted <ANT1>
 F:2-1511,1675-1881/Product: ankyrin 2.2, erythrocyte status predicted <ANT2>
 F:2-827/Region: anion exchange protein binding
 F:44-76/Domain: ankyrin repeat homology <AN02>
 F:77-109/Domain: ankyrin repeat homology <AN03>
 F:110-142/Domain: ankyrin repeat homology <AN03>
 F:143-111/Domain: ankyrin repeat homology <AN04>
 F:172-204/Domain: ankyrin repeat homology <AN05>
 F:205-237/Domain: ankyrin repeat homology <AN06>
 F:238-270/Domain: ankyrin repeat homology <AN07>
 F:271-303/Domain: ankyrin repeat homology <AN08>
 F:304-336/Domain: ankyrin repeat homology <AN09>
 F:337-369/Domain: ankyrin repeat homology <AN10>
 F:370-402/Domain: ankyrin repeat homology <AN11>
 F:403-435/Domain: ankyrin repeat homology <AN12>
 F:436-468/Domain: ankyrin repeat homology <AN13>
 F:469-501/Domain: ankyrin repeat homology <AN14>
 F:502-534/Domain: ankyrin repeat homology <AN15>
 F:535-567/Domain: ankyrin repeat homology <AN16>
 F:568-600/Domain: ankyrin repeat homology <AN17>
 F:601-633/Domain: ankyrin repeat homology <AN18>
 F:634-666/Domain: ankyrin repeat homology <AN19>
 F:667-699/Domain: ankyrin repeat homology <AN20>
 F:700-732/Domain: ankyrin repeat homology <AN21>
 F:733-765/Domain: ankyrin repeat homology <AN22>
 F:766-798/Domain: ankyrin repeat homology <AN23>
 F:828-1382/Domain: 62K status predicted <DOM2>
 F:828-1382/Region: spectrin binding
 F:1383-1881/Domain: 55K status predicted <DOM3>
 Query Match 9.3%; Score 121.5; DB 1; Length 1881;
 Best Local Similarity 27.2%; Pred. No. 0.3;
 Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;
 Oy 137 GAAGGEBDCAAFVNCNCKRRLAROLKSDTKIDSDRPRNLTERRVRESLRIM 196
 Db 1395 GSLSGTEQAEKRMVISHLDELISVAELARELFQSFEDINRRVNPNSLILDSVALILM 1454
 Oy 197 KTEKENATVAHLVGLALSCQNTLVADLVQ-EVQOARDLQ-----NRSGAMSPMSNSD 249
 Db 1455 VIRGQANMENTITALLQSIDRGELVNLBEGSGSRNLKFDKRRITDIDYLSISQANGR 1514
 Oy 250 ASTSE 254
 Db 1515 SSIOD 1519

RESULT 5
 S37771
 ankyrin, erythrocyte - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
 C:Accession: S37771
 R.Bitkemeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
 J. Biol. Chem. 268, 9533-9540, 1993
 A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found
 A:Reference number: S37771; MUID:93252825; PMID:8486643
 A:Accession: S37771
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1848 <BIR>
 A:Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:48-80/Domain: ankyrin repeat homology <AN01>
 F:81-113/Domain: ankyrin repeat homology <AN02>
 F:114-146/Domain: ankyrin repeat homology <AN03>
 F:147-175/Domain: ankyrin repeat homology <AN04>
 F:176-208/Domain: ankyrin repeat homology <AN05>
 F:209-241/Domain: ankyrin repeat homology <AN06>
 F:242-274/Domain: ankyrin repeat homology <AN07>
 F:275-307/Domain: ankyrin repeat homology <AN08>
 F:308-340/Domain: ankyrin repeat homology <AN09>
 F:341-373/Domain: ankyrin repeat homology <AN10>
 F:374-406/Domain: ankyrin repeat homology <AN11>
 F:407-439/Domain: ankyrin repeat homology <AN12>
 F:440-472/Domain: ankyrin repeat homology <AN13>
 F:473-505/Domain: ankyrin repeat homology <AN14>
 F:506-538/Domain: ankyrin repeat homology <AN15>
 F:539-571/Domain: ankyrin repeat homology <AN16>
 F:572-604/Domain: ankyrin repeat homology <AN17>
 F:605-637/Domain: ankyrin repeat homology <AN18>
 F:638-670/Domain: ankyrin repeat homology <AN19>
 F:671-703/Domain: ankyrin repeat homology <AN20>
 F:704-736/Domain: ankyrin repeat homology <AN21>
 F:737-769/Domain: ankyrin repeat homology <AN22>
 F:770-802/Domain: ankyrin repeat homology <AN23>
 Query Match 9.0%; Score 117.5; DB 2; Length 1848;
 Best Local Similarity 27.9%; Pred. No. 0.62;
 Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;
 Oy 151 VICDVGDMWRRLAOLKVSDFKIDSDRPRNLTERRVRESLRIMKTEKENATVAHLV 210
 Db 1421 VIREHGLSVAELARELFQSFEDINRRVNPNSLILDSVALILM 1480
 Oy 211 GALSQNTLVADLVQ-EVQOARDLQ-----NRSGAMSPMSNSDASTSE 254
 Db 1481 TALRIDRSEIYNMLEVSGSRNLKPERRRDREYLSIPSQVNGYSIOD 1531
 RESULT 6
 149502
 ankyrin - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: 149502
 R.White, R.A.; Bitkemeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
 Mamm. Genome 3, 281-285, 1992
 A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory
 A:Reference number: 149502; MUID:92245717; PMID:1386265
 A:Accession: 149502
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1862 <RBS>
 A:Cross-references: GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940
 C:Genetics:
 A:Gene: Ank-1
 C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing
 F:40-72/Domain: ankylrin repeat homology <AN01>
 F:73-105/Domain: ankylrin repeat homology <AN02>
 F:106-138/Domain: ankylrin repeat homology <AN03>
 F:139-167/Domain: ankylrin repeat homology <AN04>
 F:168-200/Domain: ankylrin repeat homology <AN05>
 F:201-223/Domain: ankylrin repeat homology <AN06>
 F:224-266/Domain: ankylrin repeat homology <AN07>
 F:267-299/Domain: ankylrin repeat homology <AN08>
 F:300-332/Domain: ankylrin repeat homology <AN09>
 F:333-365/Domain: ankylrin repeat homology <AN10>
 F:366-398/Domain: ankylrin repeat homology <AN11>
 F:399-431/Domain: ankylrin repeat homology <AN12>
 F:432-464/Domain: ankylrin repeat homology <AN13>
 F:465-497/Domain: ankylrin repeat homology <AN14>
 F:498-530/Domain: ankylrin repeat homology <AN15>
 F:531-563/Domain: ankylrin repeat homology <AN16>
 F:564-596/Domain: ankylrin repeat homology <AN17>
 F:597-629/Domain: ankylrin repeat homology <AN18>
 F:630-662/Domain: ankylrin repeat homology <AN19>
 F:663-695/Domain: ankylrin repeat homology <AN20>
 F:696-728/Domain: ankylrin repeat homology <AN21>
 F:729-761/Domain: ankylrin repeat homology <AN22>
 F:762-794/Domain: ankylrin repeat homology <AN23>

Query Match 9.0%; Score 117.5; DB 2; Length 1862;
 Best Local Similarity 27.9%; Pred. No. 0.62;
 Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;

OY 151 VICNVGKDMRLARLQKVSPTKIDSIEDRYPRNLTEVRSLTKMKTEKENVVHLV 210
 DB 1405 VIRHHLDSNAELARELQFSTEDINRIVENPNSLLQSTLTLWLWDREENAKMENTLY 1464
 OY 211 GALSRCOMNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWNSDASTSE 254
 DB 1465 TALRNIDRSEIVNLTGSGRSRLKPKERRRGDRREYSLSPQVNGYSLQD 1515

RESULT 7
 149299
 Receptor interacting protein RIP - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
 C:Accession: I49299
 R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
 Cell 81, 513-523, 1995
 A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
 A:Reference number: A56913; MUID:95277838; PMID:7538908
 A:Accession: I49299
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-656 <RES>
 A:Cross-references: EMBL:U25995; NID:9829618; PIDN:AA60487.1; PID:9829619
 C:Genetics:
 A:Gene: RIP
 A:Superfamily: protein kinase homology
 F:15-293/Domain: protein kinase homology <KIN>

Query Match 8.9%; Score 115.5; DB 2; Length 656;
 Best Local Similarity 34.9%; Pred. No. 0.24; Indels 3; Gaps 3;

Matches 29; Conservative 22; Mismatches 29; Indels 3; Gaps 3;
 OY 150 NVICDNGKDMRLARLQKVSPTKIDSIEDRYPRNLTEVRSLTKMKTEKENVVHLV 207
 DB 573 NPIRENIGRQMKNCARLKGFTESQIDEIDHYERDGLKEKYOMLQKWLMEGKATVG 632
 OY 208 HLVGAL-RSCOMNLVADLVQEVQ 229
 DB 633 KLAQALHQCRIIDLNLHLIRASQ 655

RESULT 8
 109479

serine/threonine protein kinase (EC 2.7.1.1-) RIP - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
 C:Accession: T09479; I38992
 R:Huang, J.; Hsu, H.; Balchwal, V.R.; Goeddel, D.V.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: Z1685
 A:Accession: T09479
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-671 <HVA>
 A:Cross-references: EMBL:U50062; NID:93426026; PID:93426027
 R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
 Cell 81, 513-523, 1995
 A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
 A:Reference number: A56913; MUID:95277838; PMID:7538908
 A:Accession: I38992
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 300-513; S', 515-671 <RES>
 A:Cross-references: EMBL:U25994; NID:9829616; PIDN:AA650137.1; PID:9829617
 C:Genetics:
 A:Gene: RIP
 C:Keywords: ATP binding; phosphotransferase

Query Match 8.6%; Score 111.5; DB 2; Length 671;
 Best Local Similarity 36.4%; Pred. No. 0.51;
 Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;

OY 152 ICDNVGKDMRLARLQKVSPTKIDSIEDRYPRNLTEVRSLTKMKTEKENVVHLV 209
 DB 590 IRENIGRQMKNCARLKGFTESQIDEIDHYERDGLKEKYOMLQKWLMEGKATVG 649
 OY 210 VGALRSC-OMNLVADLV 225
 DB 650 AQAALHQCRIIDLNLHLIRASQ 666

RESULT 9
 715347
 ankylrin-related unc-44 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Aug-2002
 C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
 R:Gallung, S.
 submitted to the EMBL Data Library, February 1996
 A:Description: The sequence of C. elegans cosmid B0350.
 A:Reference number: Z18332
 A:Accession: T15347
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2039 <GAT>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208873; PIDN:AAA93443.1
 A:Accession: T15346
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1000; 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, '32', 'S', 2034-2035, 'GSPTRRVEEHRSHQHEHGE' <GAT>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208875; PIDN:AAA93445.1
 A:Accession: T15344
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSP', 1916-1917, 'ORSTVAESTSEQVE', 1934-1935 <GAT>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208874; PIDN:AAA93444.1
 A:Accession: T15345
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, '1956-1957, 'EK PRRSVEPEHRSHQHEHGE' <GAT>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208876; PIDN:AAA93446.1
 R:Otsuka, A.J.; Franco, R.; Yang, B.; Shm, K.H.; Tang, L.Z.; Zhang, Y.X.; Boontreku
 J. Cell Biol. 129, 1081-1092, 1995

A:Title: An ankrylin-related gene (unc-44) is necessary for proper axonal guidance in *Cad*
 A:Reference number: A57282; MUID:95263663; PMID:7744957
 A:Accession: A57282
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-852; GGG, 856-1000, 'SKLOHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KME
 'SHED', 2007-2008, 'TT', 2011, 2017, 'TT', 2020-2022, 'SHIS', <OTS>
 A:Cross-references: GB:U21734; NID:9790607; PIDN:AAA85854.1; PID:9790608
 A:Accession: B57282
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 831-852, 'GG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KMEELNRL', 1727, 1799, 'E
 V', 1945-1947, 'VT', 1950, 'SG', 1975, 'SESP', 1980-1981, 'SPTRSRVPEEHRHS', 1984-1985, 'EDHES', 1
 A:Cross-references: GB:U21731
 A:Accession: C57282
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 194, 'E', 196, 'T', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, 'A
 4, 'RTV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EOS', 1939, 'ESES', 1944, 'REDDGRTVTT', 194
 A:Cross-references: GB:U21732; NID:9790603; PIDN:AAA85853.1; PID:9790604
 C:Genetics:
 A:Gene: C57282-unc-44
 A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
 C:Superfamily: ankrylin; ankrylin repeat homology
 F:164-192/Domain: ankrylin repeat homology <AN04>
 F:358-390/Domain: ankrylin repeat homology <AN11>
 F:391-423/Domain: ankrylin repeat homology <AN11>

Query Match 7.98; Score 103; DB 2; Length 2039;
 Best Local Similarity 31.98; Pred. No. 9.9;
 Matches 30; Conservative 15; Mismatches 41; Indels 8; Gaps 3;

Oy 152 ICDNVGDMRLAQLAVSDTKIDIEDRYRNLFERNRESLTKNKTEKNATVAHVYG 211
 Db 1504 VLAIGADWPLGALPHRDIOHIONTP--GQCKNTLTKIWHKEDANODINDQ 1560
 Oy 212 ALRSCOMNLVADVOEQOARD--LQNRSGAMSP 243
 Db 1561 ALRQIGRD--DIVRSTAYGEPDALLINVSQADSP 1591

RESULT 10
 F83257
 hypochelical protein PA315 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83257
 R:Stover, C.K.; Plam, X.Q.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; Llm,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:2043737; PMID:10984043
 A:Accession: F83257
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-919 <STO>
 A:Cross-references: GB:AE004735; GB:AE004091; NID:9949216; PIDN:AA06503.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA315

Query Match 7.68; Score 99; DB 2; Length 919;
 Best Local Similarity 23.68; Pred. No. 7.4;
 Matches 65; Conservative 32; Mismatches 108; Indels 70; Gaps 11;

Oy 24 ARAEPTREGARRAGPQPRPL--ADPAMPFLVILSVSSLSSELT-----LK 72
 Db 145 APVAPRATGAPAPAPAPVPTAPAGSDYRTVSDYLTMEINORNTDVSVPQATLA 204
 Oy 73 F--LCGRVYKRLERVOGSDLPMLLEONDLPEGTEILLRELLASLRHDLRLRYDDF 130
 Db 205 FOELNPGAFVGNINRLKSG-QVLRIPTEQOMLERSPREALSGVQAQNSVRGSRNPAAG 263

Oy 131 EAGA-----AAGAAGEEDCAAFNYI-----CDNNGK-DWRRLAQLKYSKD 171
 Db 264 SAGAROLDATORMAGSAPSKVYDADTNRLVSGEGRKSGADKGRGSKAIDTLAVTK 323
 Oy 172 TKIDIEDRYRNLFERNRESLRTKNTKENATVAHVGLRSCOMNLVADVOEQO 231
 Db 324 ESDLS-----TRRN---EELQSMQDLOSL--DKLOKTLQL 356
 Oy 232 RDLD-----NRGAMSPMSWNSDASTSEAS 256
 Db 357 KDAQLAKLQGLGLEGGAAPNALPDASQPNMA 391

RESULT 11
 T30934
 myosin-like protein - Parascaris univalens
 C:Species: Parascaris univalens
 C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
 C:Accession: T30934
 R:Esteban, M.R.; Giovannazzo, G.; de la haza, A.; Goday, C.
 J. Cell Sci. 111, 723-735, 1998
 A:Title: PDM1: a novel protein that associates with the centrosomes, spindle and cen
 A:Reference number: 220936; MUID:98139561; PMID:9472001
 A:Accession: T30934
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1955 <EST>
 A:Cross-references: EMBL:AF009623; NID:93068589; PID:93068590; PIDN:AAC38995.1
 C:Genetics:
 A:Note: punal

Query Match 7.68; Score 99; DB 2; Length 1955;
 Best Local Similarity 23.68; Pred. No. 19;
 Matches 52; Conservative 30; Mismatches 76; Indels 62; Gaps 9;

Oy 59 VSSLSSELEFLCIGRVYKRLER-----VOSGLDFSLMLBONDLEPH- 107
 Db 1367 VISFEDRRKVELLSKKEKLSOEELKORDERRRLKKNITVFLEAKNAQIHTL 1486
 Oy 108 TELRELLASLRHD-----LLRYVDFEAG-----AAGAAGEEDCAAFNYICD 154
 Db 1427 NDILKRVQAELENSQNDNRALRENOEQETRIHLEORLPDEGEPRYKALMAAFATERQ 1486
 Oy 155 NVGKDMRLAQLAVSDTKIDIED--RYRNL--TERVRESLRIMKTEKNATVAHL 209
 Db 1487 SLSSSLKRLASQLOISERKNDLDRDAERLKRDLKERVEDELR----- 1531
 Oy 210 VGLRSCOMNLV--ADVQEQOARD-----DLQNRSG 239
 Db 1532 -----RNLVEQTEIRENQOLRSQLGVAQSDLANSG 1563

RESULT 12
 S37431
 ankrylin 2, neuronal long splice form - human
 N:Alternate names: ankrylin B, 440K splice form; ankrylin-B; brain ankrylin; non-erythro
 N:Contains: ankrylin 2, short form
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
 R:Chan, W.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37431
 A:Accession: S37431
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-3924 <CHA>
 A:Cross-references: EMBL:Z26634; NID:9406287; PIDN:CAAB1387.1; PID:9406288
 R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A:Title: Isolation and characterization of cDNAs encoding human brain ankrylins reveal
 A:Reference number: A39643; MUID:91302466; PMID:1830053

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Query Match          7.6%; Score 99; DB 2; Length 3924;
Best Local Similarity 23.98; Pred. No. 47;
Matches      32; Conservative    25; Mismatches   59; Indels    18; Gaps     3;

0Y      LTRRVDPDEAAGAAGAPGEED--LCAAFNYICDNVGKDRRLARQLKAVSDPKIDSIEDR 180
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      3513 LIERIPD-ENSHDDAEEDPQDEQRIEERLAYIAHLGFSWEELAREIDFTEQHIOIRIE 3571Y
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      YPRULTEVRSESLTKMKTETKENMTVAHLYGALNSCCNNLVADLYQ----- 226
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      3572 NPNSLLQDOSYLKLWIERDEGRKHATDTNLVECLTRINMDIVYHMETPELOERISHSY 3631Y
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      EYQQARDLNRRSG 239
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Query Match 7.6%; Score 98.5; DB 1; Length 4644;
Best Local Similarity 23.5%; Pred. No. 64;
Matches 59; Conservative 32; Mismatches 83; Indels 77; Gaps 12;

OY 53 LVLLHSVSSSSLSSELTFLKFLCGRVYKRLERYOSGL-----DL 93
Db 376 LRLVLAESIRDLSSQLTKLVGTBKLMHVAEEFEKVMACFEVFOTMDDEYERLOVLLNDI 435
OY 94 FSMLEON-----DLEPGHTEL---LRELTLSTRHDLR---RVDDFEAGAAA---G 137
Db 436 VKRRREELKWKVIRNPAPHRKLOARLDQMKFRPHOEBLRAVIRYVLRPOTVAAGQNG 495
OY 138 AAPGEEDICAA-----FNVICDNV---GKD-----WRRLARQLKYSV 171
Db 496 EAPFPQDKVAEVLFDADANAIEEVLNLAENKVEVDGLDYSKEGTEAME---AAMKRYD 552
OY 172 TKDISIERYRNRLTERVRESRLTMKN-----EKENATVA---HLVGALRSCOMNLYA 222
Db 553 ERIDRVER---TLARLDQLGTAKNANEMKFRITFSRNALFVRPHINGALREYOTOLIQ 608
OY 223 DLVQEVQCARD 233
Db 609 RVKQDIESLMD 619

RESULT 14
A84290
Glu-rRNA amidotransferase [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84290
R:Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
R.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.;

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Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of *Halobacterium* species NRC-1.
 A:Reference number: A84160; MID:20504483; PMID:11016950
 A:Accession: A84290
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-622 <STO>
 A:Cross-References: GB:AE004437; NID:g10580865; PIDN:AAG19685.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: gatB1

Query Match 7.5%; Score 97; DB 2; Length 622;

Best Local Similarity 24.3%; Pred. No. 6.5;
 Matches 64; Conservative 31; Mismatches 96; Indels 72; Gaps 14;

QY 17 LGRRDLARASEP-RTEGARRAGPP-PPLAD-----PANDPVLVLSVSSL 63
 DB 391 VAEKRTAMAGVPEETRGANDGTSTKYLPLGAAAMPETDVPYDP-----DP 440
 QY 64 SSELTEFLCLGKRVKKRLERVOGGLDFSKLLEQ-----NDLEPG-----H 107
 DB 441 SAVERPEL-----LTKEVERYQADFLDAGLAQVAYGRRQLFEQOVEAGVDATLA 492
 QY 108 TELRLRLASLRHDL-LRVDDFEAGAAAG-----AAGGEDICAAFNVCNVDGKD 159
 DB 493 AQLTESTVTELRRDDVPVGLTDHFRGYLGIVADGLAQEGVPELLAA---LAEPGSD 549
 QY 160 WRRLAROLKVSPTKIDSIDR---YPRNLTERVRESLRIMKTEKENATVAHLVGALRS 215
 DB 550 PAVLAEELGLGSAEDVEAVYGVYERNSDOVAAGKGAFA-----SALMEGCMGALRG 603
 QY 216 COMNLVADLYOEVOCAADLQNRS 238
 DB 604 ---KADGDLVSEYLR-EEIQORS 622

RESULT 15

T49191

hypothetical protein MAA21.130 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49191

R:Reger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K

submitted to the Protein Sequence Database, April 2000

A:Reference number: 225018

A:Accession: T49191

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1162 <RIE>

A:Cross-References: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.130

A:Experimental source: cultivar Columbia; BAC clone MAA21

C:Genetics:

A:Gene: ATSP:MAA21.130

A:Map position: 3

A:introns: 975/1

C:Superfamily: Arabidopsis thaliana hypothetical protein MAA21.130

Query Match 7.4%; Score 96.5; DB 2; Length 1162;

Best Local Similarity 22.6%; Pred. No. 16;

Matches 59; Conservative 35; Mismatches 98; Indels 69; Gaps 12;

QY 8 REGG-----GILGPIGKRRDLARASEPTEGARRAGPOPPPLAD 46
 DB 108 REGGPNDRGVDDRDRLDAERDRLKSPSWRSDSPNELSKFKPLDSRNSRSKSLAS 167
 QY 47 PANDPVLVLSVSSLSELTEFLCLGKRVKKRLERVOGGLDFSKLLEQNDLEPG 106
 DB 168 PTW-----SKDSGSEQSK---SVGNVYKKSSEEVQCKSSSTTSSEMEGELEPE 212
 QY 107 HTLELLRLASLRHDL-----RVVD-DF-EAGAAAGAAGGEDICAAFNVIC 153

DB 213 PQPETAAGLAHQTKHKCKLPSCSADHKNAIDRSFOEIGKSA-----QLDANTESNREL 267
 QY 154 DNYGDMRLAROLKVSPTKID--STEDRIPKRLTERVRESLRIMKTEKENATVA---- 207
 DB 268 SHVGGN-----REMETTDSMTDKSYED--AENVPEHAESMHSVSONNNDSTALAIH 320
 QY 208 -HLVGAIRSCOMNLVADLYOE 227
 DB 321 DHRDGTI-TASANKITDLYDE 340

Search completed: June 19, 2003, 10:39:08
 Job time : 21 secs

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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:29:05 ; Search time 22 seconds

(without alignments)
482,634 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNOAPECRGCGGILGPKR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1040	79.9	208 1	FADD_HUMAN
2	719.5	55.3	205 1	FADD_MOUSE
3	122	9.4	479 1	ICEB_HUMAN
4	121.5	9.3	1880 1	ANK1_HUMAN
5	117.5	9.0	1862 1	ANK1_MOUSE
6	115.5	8.9	656 1	R1K1_MOUSE
7	111.5	8.6	671 1	R1K1_HUMAN
8	110	8.4	480 1	CFLA_HUMAN
9	108	8.3	521 1	ICEA_HUMAN
10	99	7.6	3924 1	ANK2_HUMAN
11	98.5	7.6	4644 1	DTHC_MOUSE
12	98.5	7.6	4644 1	DTHC_RAT
13	96.5	7.4	535 1	HTR1_HUMAN
14	95.5	7.3	497 1	RP54_PSEAE
15	93.5	7.2	324 1	TNR6_RAT
16	92	7.1	381 1	T10B_MOUSE
17	91.5	7.0	470 1	ANK1_MOUSE
18	91.5	7.0	1816 1	ANK1_MOUSE
19	91	7.0	3695 1	IMAA4_HUMAN
20	90.5	7.0	130 1	PE15_MOUSE
21	90.5	7.0	411 1	KICL_MOUSE
22	90	6.9	295 1	X769_HUMAN
23	90	6.9	953 1	YAA2_HUMAN
24	89.5	6.9	535 1	HTR1_HUMAN
25	89.5	6.9	962 1	ARVQ_HUMAN
26	89	6.8	429 1	AS10_HUMAN
27	89	6.8	483 1	KICL_MOUSE
28	88.5	6.8	130 1	PE15_MOUSE
29	88.5	6.8	892 1	ANK1_HUMAN
30	88.5	6.8	893 1	ANK1_HUMAN
31	87.5	6.7	433 1	CGBI_HUMAN
32	87.5	6.7	484 1	CFLA_MOUSE
33	87.5	6.7	759 1	EPLI_HUMAN

34	87.5	6.7	894 1	AAQ2_MOUSE	091191 mus musculus
35	87.5	6.7	3433 1	UTRO_HUMAN	P46933 homo sapien
36	87.5	6.7	4377 1	ANK2_HUMAN	Q12955 homo sapien
37	87	6.7	332 1	TNR6_PIG	077736 sus scrofa
38	86.5	6.6	294 1	PABR_CAUCR	005190 caulobacter
39	86.5	6.6	1073 1	MTR4_YEAST	P47047 saccharomyc
40	86	6.6	587 1	TCNO_HAETN	P41144 haemophilus
41	86	6.6	1453 1	Y373_BOVIN	091u23 bos taurus
42	85.5	6.6	880 1	RA50_PYRAB	09uzc8 pyrococcus
43	85	6.5	899 1	PLC1_SCHPO	P40976 schizosacch
44	84.5	6.5	892 1	AAQ1_RAT	0921p2 rattus norv
45	84.5	6.5	903 1	YB56_MERTU	058556 methanococc

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	208 AA
FADD_HUMAN	013158	Q14866			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	FADD protein (Fas-associated death domain-containing protein)				
DE	(Mediator of receptor induced toxicity)				
GN	FADD OR MORT1				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI:TaxID=9606;				
RP	SEQUENCE FROM N.A. AND MUTAGENESIS.				
RC	TISSUE=umbilical vein endothelial cells;				
RA	MEDLINE-95277837; PubMed-7538907;				
RA	Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;				
RT	"FADD, a novel death domain-containing protein, interacts with the				
RT	death domain of Fas and initiates apoptosis.";				
RL	Cell 81:505-512(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE-95229578; PubMed-7536190;				
RA	Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,				
RA	Wallach D.;				
RT	"A novel protein that interacts with the death domain of Fas/Apo1				
RT	contains a sequence motif related to the death domain.";				
RL	J. Biol. Chem. 270:7795-7798(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				
RA	Strausberg R.;				
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	STRUCTURE BY NMR OF 1-83.				
RC	MEDLINE-96241233; PubMed-9582077;				
RA	Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,				
RA	Leonard M.J., Feix S.W.;				
RT	"NMR structure and mutagenesis of the FADD (Mort1) death-effector				
RT	domain.";				
RL	Nature 392:941-945(1998).				
CC	-1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR				
CC	CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNF-R1 RECEPTORS. THE				
CC	RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX				
CC	(DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8				
CC	INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC				
CC	PROTEINASES) MEDIATING APOPTOSIS.				
CC	-1- SUBUNIT: INTERACTS WITH CFLAR.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT				
CC	FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.				
CC	-1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE				
CC	CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.				
CC	-1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).				
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.				

```

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CC -----
CC
CC EMBL; U24231; AAA86517.1; .
CC EMBL; X84709; CAA59197.1; .
CC EMBL; BC000334; AAH00334.1; .
CC PDB; 1A1W; 16-FEB-99.
CC PDB; 1A1Z; 16-FEB-99.
CC Genew; HGNC:3573; FADD.
CC DR MIM; 602457; .
CC DR InterPro; IPR001875; DED.
CC DR InterPro; IPR000488; Death.
CC DR Pfam; PF00531; death; 1.
CC DR Pfam; PF01335; DED; 1.
CC DR SMART; SM00005; DEATH; 1.
CC DR SMART; SM00031; DED; 1.
CC DR PROSITE; PSS0017; DEATH.DOMAIN; 1.
CC DR PROSITE; PSS0168; DED; 1.
CC DR Apoptosis; 3D-structure.
CC KW DOMAIN 3
CC FT 97 181 DED.
CC FT MOTAG 121 121 DEATH.
CC FT CONFLICT 32 32 V->N. NO INTERACTION WITH FAS RECEPTOR.
CC SEQUENCE 208 AA; 23279 MW; 0B65E2F852B83507 CMC64;.

```

DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE (Apoptotic protease Mch-5) (CASP4).
GN CASP8 OR MCH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Thymus, and B-cell;
RX MEDLINE=96279827; PubMed=8681376;
RA Boldin M.P., Goncharov T.M., Golitssev Y.V., Wallach D.;
RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT Fas/APO-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815 (1996).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96279827; PubMed=8681377;
RA Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA M.J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RA Kramer P.H., Peter M.E., Dixit V.M.;
RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
RL Cell 85:817-827 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Frits L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493;
RA Grenet J., Teliez T., Mel T., Valentine V., Kidd V.J.;
RT "Structure and chromosome localization of the human CASP8 gene.";
RL Gene 226:225-232 (1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
RX MEDLINE=97373533; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., O'Tillie S., Bullrich F., Banks S.,
RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545 (1997).
RN [6]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
RN [7]
RP FUNCTION.
RX MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
RN [8]
RP PROCESSING.
RX MEDLINE=97373557; PubMed=9184224;
RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing

RT signaling complex (DISC).";
RL EMBL J. 16:2794-2804 (1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Grutter M.G.;
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133 (1999).
CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
CC TNFR-1 INDUCED CELL DEATH. BINDING TO THE APOFOR MOLECULE FADD
CC RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED
CC THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
CC LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC
CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE
CC (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC.
CC CLEAVES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY
CC PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-
CC MOLECULE SUBSTRATE, AC-ASP-GIT-VAL-ASP-1-AMC. LIKELY TARGET FOR
CC THE COMPOX VIRUS CRMA DEATH INHIBITOR PROTEIN.
CC -1- SUBUNIT: HETERODIMER OF A 18 KDA (P18) AND A 10 KDA (P10) SUBUNIT.
CC INTERACTS WITH CELFAR.
CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS: 1-ALPHA (SHOWN HERE), 2-
CC ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-
CC BETA. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN A
CC WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD
CC LEUCOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN,
CC TESTIS, AND SKELETAL MUSCLE.
CC -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE
CC DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE
CC AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND
CC CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
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CC
CC EMBL: X98172; CAA66853.1;
CC EMBL: X98173; CAA66854.1;
CC EMBL: X98174; CAA66855.1;
CC EMBL: X98175; CAA66856.1;
CC EMBL: X98176; CAA66857.1;
CC EMBL: X98177; CAA66858.1;
CC EMBL: X98178; CAA66859.1;
CC EMBL: U58143; AAC50602.1;
CC EMBL: U60520; AAC50645.1;
CC EMBL: AF102144; AAD24962.1;
CC EMBL: AF102139; AAD24962.1;
CC EMBL: AF102140; AAD24962.1;
CC EMBL: AF102141; AAD24962.1;
CC EMBL: AF102142; AAD24962.1;
CC EMBL: AF102143; AAD24962.1;
CC EMBL: AF102144; AAD24962.1;
CC EMBL: AF102145; AAD24962.1;
CC EMBL: AF009620; AAB70913.1;
CC PDB: 1ODU; 10-JUL-00.
CC MEROPS: C14-009;
CC Genew: HGNC:1509; CASP8.
CC MIM: 601763;
CC InterPro: IPR001875; DED.
CC InterPro: IPR002138; ICE_P10.
CC InterPro: IPR001309; ICE_P20.

DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR Pfam; PF01335; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 DR Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;
 KW Repeat; 3D-structure.
 FT PROPEP 1 216
 FT CHAIN 217 374 CASPASE-8 SUBUNIT P18.
 FT PROPEP 375 384
 FT CHAIN 385 479 CASPASE-8 SUBUNIT P10.
 FT ACCT SITE 317 317
 FT ACCT SITE 360 360
 FT DOMAIN 2 80
 FT DOMAIN 100 177
 FT VASAPLIC 102 102
 FT VASAPLIC 184 198
 FT VASAPLIC 184 220
 FT VASAPLIC 184 267
 FT VASAPLIC 199 235
 FT VASAPLIC 221 479
 FT VASAPLIC 236 479
 FT VASAPLIC 269 276
 FT VASAPLIC 277 479
 FT CONFLICT 285 285
 FT CONFLICT 294 294
 FT CONFLICT 331 331
 FT SEQUENCE 479 AA; 55391 MW; 7A5FEA6B39B582P CRC64;
 Query Match 9.4%; Score 122; DB 1; Length 479;
 Best Local Similarity 28.8%; Pred. No. 0.025;
 Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;
 Oy 56 LHSVSSLSSELELKLCLGRVYKRLERVOGLDFMLLEGNLDPGHTTELLRELL 115
 Db 7 LYDIGEQLDSEDLASLKLFLDYIPQRKEPIKDALMFORLOERMLSESNLSFLKELL 66
 Oy 116 ASLRHRL-----RYDDFAGAGAAAGPEEDLCAFNVICNVGDMRR-----L 163
 Db 67 FRIRRLDLITYLNTREMEREL--QTGPAQI-SAYRVMLYQISEVSRSSELSRPF 122
 Oy 164 AROLKVSPTKID 175
 Db 123 LLOEISKCKID 134
 RESULT 4
 ID ANK1_HUMAN STANDARD: PRT; 1880 AA.
 AC P16157;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).
 GN ANK1 OR ANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
 RC TISSUE=Hematopoietic;

RX MEDLINE-90158830; PubMed-2137557;
 RA Lux S.E., John K.M., Bennett V.;
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 structure with homology to tissue-differentiation and cell-cycle
 control proteins.";
 RT Nature 344:36-42(1990).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90175370; PubMed-1689849;
 RA Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Spelcher D.,
 RA Cheung M.C., Kan Y.W., Palek J.;
 RT "cDNA sequence for human erythrocyte ankyrin.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
 RL [3]
 RP VARIANT HS ILE-462.
 RX MEDLINE-96225450; PubMed-8640229;
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
 RA Dornwell M., Hebers J., Kugler W., Oezcan R., Pekrun A.,
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive
 hereditary spherocytosis.";
 RT Nat. Genet. 13:214-218(1996).
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
 ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
 CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CYTOSKELETAL DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: CYTOSOL; SURFACE OF ERYTHROCYTIC
 PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1/2.1 (shown here),
 2/2.2 and 3; are produced by alternative splicing.
 CC -1- PTM: REGULATED BY PHOSPHORYLATION.
 CC -1- PTM: ACTIVATED BY PALMITIC ACID GROUP(S).
 CC -1- DISEASE: Defects in ANK1 are the cause of dominant and recessive
 hereditary spherocytosis (HS).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X16609; CA34610.1; -;
 DR EMBL; M28880; AA51732.1; -;
 DR PIR; S08275; SJHOK.
 DR PIR; A35049; A35049.
 DR HSSP; 000420; IAWC.
 DR GeneW; HGNC:492; ANK1.
 DR MIM; 182900; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000906; ZUS.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 22.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.
 DR PROSITE; PS50086; ANK_REPEAT; 20.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;
 KW Polymorphism.
 FT INIT_MET 0 0
 FT DOMAIN 1 826 89 KDA DOMAIN (ANION EXCHANGE PROTEIN

```

FT  DOMAIN  827  1381  BINDING DOMAIN).
FT  DOMAIN  1382  1880  62 KDA DOMAIN (SPECTRIN BINDING
FT  REPEAT  43  72  55 KDA REGULATORY DOMAIN (REGULATES
FT  REPEAT  76  105  THE BINDING OF ANKYRIN TO SPECTRIN
FT  REPEAT  109  138  AND THE BAND 3 PROTEIN).
FT  REPEAT  142  171  ANK 1.
FT  REPEAT  173  200  ANK 2.
FT  REPEAT  204  233  ANK 3.
FT  REPEAT  237  266  ANK 4.
FT  REPEAT  270  299  ANK 5.
FT  REPEAT  303  332  ANK 6.
FT  REPEAT  336  365  ANK 7.
FT  REPEAT  369  398  ANK 8.
FT  REPEAT  402  431  ANK 9.
FT  REPEAT  435  464  ANK 10.
FT  REPEAT  468  497  ANK 11.
FT  REPEAT  501  530  ANK 12.
FT  REPEAT  534  563  ANK 13.
FT  REPEAT  567  596  ANK 14.
FT  REPEAT  600  629  ANK 15.
FT  REPEAT  633  662  ANK 16.
FT  REPEAT  666  695  ANK 17.
FT  REPEAT  699  728  ANK 18.
FT  REPEAT  732  761  ANK 19.
FT  REPEAT  765  794  ANK 20.
FT  DOMAIN  1402  1486  ANK 21.
FT  VARSPIC  1512  1874  MISSING (IN ISOFORM 2).
FT  VARSPIC  1849  1880  H -> D (IN ISOFORM 2).
                          TVEGDLPESELEDDYFKHSHDHTSTNP -> ELRGS
                          GLOPDLGKRGKQAVARALKRKGQ (IN ISOFORM
                          3).
FT  VARIANT  20  20  R -> T.
                          /FtId-VAR_000595.
FT  VARIANT  462  462  V -> I (IN HS).
                          /FtId-VAR_000596.
FT  VARIANT  618  618  R -> H (IN BRUGSEN).
                          /FtId-VAR_000597.
FT  VARIANT  749  749  V -> A.
                          /FtId-VAR_000598.
FT  VARIANT  844  844  D -> E.
                          /FtId-VAR_000599.
FT  VARIANT  1285  1285  E -> D.
                          /FtId-VAR_000601.
FT  VARIANT  1391  1391  S -> T.
                          /FtId-VAR_000600.
FT  VARIANT  1591  1591  D -> N (IN DUESSELDORF).
                          /FtId-VAR_000602.
FT  VARIANT  1698  1698  R -> D.
                          /FtId-VAR_000603.
FT  CONFLICT  229  229  A -> S (IN REF. 2).
FT  CONFLICT  1545  1545  V -> I (IN REF. 2).
FT  SEQUENCE  1880 AA; 206145 MW; 1CSF5E7EPD1CD428 CRC64;
SQ
Query Match 9.3%; Score 121.5; DB 1; Length 1880;
Best Local Similarity 27.2%; Pred. NO. 0.15; Indels 7; Gaps 2;
Matches 34; Conservative 28; Mismatches 56;

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RESULT 5
AN1 MOUSE STANDARD: PRT; 1862 AA.
ID ANK1_MOUSE
AC 002357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Ankyrin 1 (Erythrocyte ankyrin).
GN ANK1 OR ANK-1
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Erythrocyte;
RX MEDLINE=92343717; PubMed=1386265;
RA White R.A., Birkmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
RT regulatory domain."
RL Mamm. Genome 3:281-285(1992).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2; TO
CC NA-K ATPASE; TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85; AND TO THE
CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
CC PLASMA MEMBRANE.
CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: ACETYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
CC -----
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CC -----
DR EMBL; M84756; AAA37236.1;
DR HSSP; 000420; IAWC.
DR MGD; MGI:88024; Ank1.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR SMART; SM00248; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
DR 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
DR 62 KDA DOMAIN (SPECTRIN BINDING
DR 55 KDA REGULATORY DOMAIN (REGULATES
DR THE BINDING OF ANKYRIN TO SPECTRIN
DR AND THE BAND 3 PROTEIN).
FT  DOMAIN  828  1386  ANK 1.
FT  DOMAIN  1387  1862  ANK 2.
FT  REPEAT  40  69  ANK 3.
FT  REPEAT  73  102  ANK 4.
FT  REPEAT  106  135  ANK 5.
FT  REPEAT  139  168  ANK 6.
FT  REPEAT  170  197  ANK 7.

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FT REPEAT 201 230 ANK 6.
 FT REPEAT 224 263 ANK 7.
 FT REPEAT 267 296 ANK 8.
 FT REPEAT 267 296 ANK 8.
 FT REPEAT 300 329 ANK 9.
 FT REPEAT 333 362 ANK 10.
 FT REPEAT 366 395 ANK 11.
 FT REPEAT 399 428 ANK 12.
 FT REPEAT 432 461 ANK 13.
 FT REPEAT 465 494 ANK 14.
 FT REPEAT 498 527 ANK 15.
 FT REPEAT 531 560 ANK 16.
 FT REPEAT 564 593 ANK 17.
 FT REPEAT 597 626 ANK 18.
 FT REPEAT 630 659 ANK 19.
 FT REPEAT 663 692 ANK 20.
 FT REPEAT 696 725 ANK 21.
 FT REPEAT 729 758 ANK 22.
 FT REPEAT 762 791 ANK 23.
 FT DOMAIN 1399 1483 DEATH.
 SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001B5 CRC64;

Query Match 9.0%; Score 117.5; DB 1; Length 1862;
 Best Local Similarity 27.9%; Pred. No. 0.3; Mismatches 44; Indels 7; Gaps 2;
 Matches 31; Conservative 29;

DB 151 VICDNVGMKRLRLKLVSDIKIDRIYPRNLTFRVRESLRINKTEKENATVAHLY 210
 1405 VIREHGLSMALRLQSVEDINIRVENPNSILDOSTALTTLTVDRGENAKKENLY 1464
 211 GALSQNMVLVDLVO-EVOQARDQ-----NRSGAMSPMNSDASTSE 254
 1465 TALNRIDREIYNMELGSGROSHNKPERRHGDREYSLSPQVNGYSSLD 1515

RESULT 6

RIKL_MOUSE
 ID RIKL_MOUSE STANDARD; PRT; 656 AA.

AC 060855;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.1-)
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
 DE (Receptor interacting protein).
 GN RIPK1 OR RIP OR RIMP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=95277838; PubMed=7538908;
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
 RT "RIP: a novel protein containing a death domain that interacts with Fas/PO-1 (CD95) in yeast and causes cell death.";
 RL Cell 81:513-523(1995).
 CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
 CC -1- TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC EMBL: U25995; AAB60487.1; -

DR HSP: P25445; 1DDF.
 DR MGD; MG1:108212; RPK1.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR pfam: PF00069; pkinase; 1.
 DR pfam: PF00531; death; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Apoptosis.
 FT DOMAIN 17 290 PROTEIN KINASE.
 FT NP_BIND 23 31 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 568 654 DEATH.
 FT VARIANT 473 473 T->I.
 SQ SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;

Query Match 8.9%; Score 115.5; DB 1; Length 656;
 Best Local Similarity 34.9%; Pred. No. 0.12; Mismatches 29; Indels 3; Gaps 3;
 Matches 29; Conservative 22;

DB 150 NVICDNVGMKRLRLKLVSDIKIDRIYPRNLTFRVRESLRINKTEKENATVA 207
 573 NPIRENGLGMKRCARLKLTESQIDEIDHVRDGLKRYQMLKMLRBSGKATG 632
 208 HLYGAL-RSCQNMVLVDLVOEVO 229
 633 KLAQALHCCCRIDLNLHLIRASQ 655

RESULT 7

RIKL_HUMAN
 ID RIKL_HUMAN STANDARD; PRT; 671 AA.

AC Q13546; Q13180;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.1-)
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
 DE (Receptor interacting protein).
 GN RIPK1 OR RIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=96200892; PubMed=8612133;
 RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF receptor-1 signaling complex.";
 RL Immunity 4:387-396(1996).
 RN [2]
 RP REVISION TO 120.
 RA Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 300-671 FROM N.A.
 RC MEDLINE=95277838; PubMed=7538908;
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
 RT "RIP: a novel protein containing a death domain that interacts with Fas/PO-1 (CD95) in yeast and causes cell death.";
 RL Cell 81:513-523(1995).
 CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-

DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC - SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 DR EMBL: U50062; AAC3232.1; -
 DR EMBL: U25994; AAC50137.1; -
 DR HSSP: P08631; 1AD5; KIPK1.
 DR Genew: H08C110019; KIPK1.
 DR MIM: 603453; -
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR Pfam: PF00531; death.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00005; DEATH.1.
 DR SMART: SM00221; STYK.1.
 DR PROSITE: PS00106; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS50017; DEATH_DOMAIN.1.
 KM Transerferase: Serine/threonine-protein kinase; ATP-binding;
 KM Apoptosis.
 FT DOMAIN 17 269 PROTEIN KINASE.
 FT NF_BIND 23 31 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 583 669 DEATH.
 FT DOMAIN 411 414 POLY-ARG.
 FT CONFLICT 514 514 T -> S (IN REF. 3).
 FT SEQUENCE 671 AA; 75958 MW; BADCAETET0456ABE CRC64;
 SQ
 Query Match 8.68; Score 111.5; DB 1; Length 671;
 Best Local Similarity 36.48; Pred. No. 0.25; Indels 3; Gaps 3;
 Matches 28; Conservative 19; Mismatches 27;
 QY 152 ICDNKGDMRRLARQLVSDTKIDSIDRYPN-ITERVESLRINTEK-ENATVAHL 209
 Db 590 IREHLGKMKNCARLFTQSQIDHDYERDLKRYKVMQLQKVMREGIKCATYGL 649
 QY 210 VGALRSC-QMNLVADLY 225
 Db 650 AQAHLHQSRIIDLSLI 666
 RESULT 8
 CELA_HUMAN STANDARD; PRT; 480 AA.
 AC O15519; O15336; O15137; O60458; O43618; O16673; O43619; O43620;
 AC O14675; O60459; O14674; O9UEWL; O15510; O15138;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
 DE Inhibitory protein) (C-FLIP) (Caspase-eight-related protein) (Casper)
 DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
 DE inducer of toxicity) (WRIT) (Caspase homologue) (CASH) (Inhibitor of
 DE FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
 DE (Usurpin).
 GN CELAR OR CLARP OR WRIT OR CASH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF
 RP TYR-360
 RC TISSUE-Embryonic Kidney, and Umbilical vein endothelial cells;
 RX MEDLINE-97352452; PubMed-9208847;
 RA Shu H.-B., Halpin D.R., Goeddel D.V.;
 RT "Casper is a FADD- and caspase-related inducer of apoptosis.";
 RL Immunity 6:751-763(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE-97470967; PubMed-9326610;
 RA Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Trask B.J.,
 RA Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;
 RT "WRIT, a novel death-effector domain-containing protein, interacts
 RT with caspases and BclXL and initiates cell death.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11133-11138(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Peripheral blood lymphocytes;
 RX MEDLINE-97360133; PubMed-9217161;
 RA Immler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
 RA Bodmer J.-L., Schroeder M., Burns K., Mattmann C., Rimoldi D.,
 RA French L.E., Tschopp J.;
 RT "Inhibition of death receptor signals by cellular FLIP.";
 RL Nature 388:190-195(1997).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF
 RP ASP-376.
 RC TISSUE-T-cell;
 RX MEDLINE-97373543; PubMed-9228018;
 RA Sriivasula S.M., Ahmad M., Oltillie S., Bullrich F., Banks S.,
 RA Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
 RA Armstrong R.C., Alnemri E.S.;
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis.";
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Umbilical vein endothelial cells;
 RX MEDLINE-97362203; PubMed-9211860;
 RA Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 RT CD-95-induced apoptosis.";
 RL J. Biol. Chem. 272:17255-17257(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RA Hu S., Dixit V.M.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE-Kidney;
 RX MEDLINE-99218584; PubMed-10200473;
 RA Rasper D.M., Vallancourt J.P., Hadano S., Houtzager V.M., Selden I.,
 RA Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
 RA Koop B.F., Peterson E.P., Thorndberry N.A., Huang J., Macpherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 RT homologue that precludes caspase-8 recruitment and activation by the
 RT CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Skin fibroblast;
 RX MEDLINE-97426025; PubMed-9289491;
 RA Goltsev Y.V., Kovalevko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Colon carcinoma;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE-BRAIN stem; PubMed-1830053;
 RX MEDLINE-91302466; PubMed-1830053;
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RT "Isolation and characterization of cDNAs encoding human brain
 ankyrins reveal a family of alternatively spliced genes."
 RL J. Cell Biol. 114:241-253(1991).
 RN [2]
 RP REVISIONS.
 RA Carpenter S.;
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-BRAIN stem; PubMed-8253844;
 RX MEDLINE-94075409; PubMed-8253844;
 RA Chan W., Kordell E., Bennett V.;
 RT "440-kD ankyrinB: structure of the major developmentally regulated
 domain and selective localization in unmyelinated axons."
 RL J. Cell Biol. 123:1463-1473(1993).
 RN [4]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE-92009921; PubMed-1833308;
 RA Tse W.T., Manninger J.C., Yang-Peng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 ankyrin gene."
 RL Genomics 10:858-866(1991).
 CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal
 elements. Also bind to cytoskeletal proteins.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CELLS THROUGHOUT THE BRAIN.
 CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 AND FUNCTION (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 between the Swiss Institute of Bioinformatics and the EMBL outstation
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 use by non-profit institutions as long as its content is in no way
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 or send an email to license@isb-sdb.ch).
 CC
 DR EMBL; X56957; CAA40278.1; -;
 DR EMBL; X56958; CAA40279.2; -;
 DR EMBL; X26634; CAA42644.1; -;
 DR EMBL; M37123; AAG62828.1; -;
 DR PIR; S14533; S14533;
 DR PIR; A39643; A39643;
 DR PIR; B39643; B39643;
 DR PIR; S14569; S14569;
 DR HSP; P42771; IDC2.
 DR GeneW; HGNC:493; ANK2.
 DR MIM; 106410; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000906; ZUS.
 DR Pfam; PF000023; ank; 24
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.

DR PROSITE; PS50086; ANK_REPEAT; 20;
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation.
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ID DYHC_MOUSE STANDARD; PRT: 4644 AA.
AC 09JHID;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Dynein heavy chain, cytosolic (DYHC) (cytoplasmic dynein heavy chain).
GN DNMCH1 OR DNMCH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FVB;
RA Sasaki S., Shionoya A., Hirotsune S.;
RT Complete cDNA sequence of murine cytoplasmic dynein heavy chain."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A
CC MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
CC ORGANELLES ALONG MICROTUBULES.
CC -1- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
CC INTERMEDIATE AND LIGHT CHAINS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC
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CC
DR EMBL; AF004877; AAF91078.1;
DR MGD; MG1:103147; Dnchcl.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PFO3028; Dynein_heavy; 1.
KM Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
FT DOMAIN 48 69
FT 179 200 COILED COIL (POTENTIAL).
FT DOMAIN 453 476 COILED COIL (POTENTIAL).
FT 541 564 COILED COIL (POTENTIAL).
FT DOMAIN 1169 1201 COILED COIL (POTENTIAL).
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FT DOMAIN 1355 1371 COILED COIL (POTENTIAL).
FT 2012 2040 COILED COIL (POTENTIAL).
FT DOMAIN 3187 3273 COILED COIL (POTENTIAL).
FT 3394 3498 COILED COIL (POTENTIAL).
FT DOMAIN 3735 3798 COILED COIL (POTENTIAL).
FT 1904 1911 COILED COIL (POTENTIAL).
FT NP_BIND 2222 2229 ATP (POTENTIAL).
FT NP_BIND 2593 2600 ATP (POTENTIAL).
FT NP_BIND 2935 2942 ATP (POTENTIAL).
SQ SEQUENCE 4644 AA; 532021 MW; FES54E15DD479E1B CRC64;

Query Match 7.68; Score 98.5; DB 1; Length 4644;
Best Local Similarity 23.58; Pred. No. 28;
Matches 59; Conservative 33; Mismatches 83; Indels 77; Gaps 12;

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DB 376 LRLVEAISRLSSGLLVLTGRKLAMHAYEEFEVYVMACEVQYTWDEYKLVLDI 435
QY 94 FSLMLEON-----DLEGHTEL--LRELASLRHDLRL--RVDFEGAAA---G 137
DB 436 VKRKRENLKMWYINPAHRLQARLDOMKRFROHQLRAVYVRLPQVTAVAQNOG 495
QY 138 AARBEELCAA-----ENVICDNV--GKD-----KRLAQLAYSD 171
DB 496 EAPPODKAEVLEDAADANTIEEVLAENEKVDGLVYSKEGTAME--AAAKRYD 552
QY 172 TKIDSIDRYPRNTEREVSRLRWNT-----EKENATVA--HLVGLARSCOMLVYA 222

DB 553 ERIDRVETR---ITARLDQGLGAKNANEMERIFSRFNLFVRPHIRGAIREQQLIO 608
QY 223 DLYOEVOQARD 233
DB 609 RYKDDIESLHD 619

RESULT 12

DYHC_RAT STANDARD; PRT: 4644 AA.
ID DYHC_RAT
AC P38650; 063178;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC) (cytoplasmic dynein heavy chain)
GN DNMCH1 OR DNMCH1 OR DNMCH1 OR MAP1C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; TISSUE-Brain;
RX MEDLINE-93376715; PubMed-7690137;
RA Zhang Z., Tanaka Y., Nonaka S., Aizawa H., Kawasaki H., Nakata T.,
RT "The primary structure of rat brain (cytoplasmic) dynein heavy chain,
RT a cytoplasmic motor enzyme."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7928-7932(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Brain;
RX MEDLINE-93264075; PubMed-7684232;
RA Mekami A., Paschal B.M., Mazumdar M., Vallee R.B.;
RT "Molecular cloning of the retrograde transport motor cytoplasmic
RT dynein (MAP 1C)."
RL Neuron 10:787-796(1993).
CC -1- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A
CC MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
CC ORGANELLES ALONG MICROTUBULES.
CC -1- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
CC INTERMEDIATE AND LIGHT CHAINS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC
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CC
DR EMBL; D13896; BAA02996.1;
DR EMBL; D08505; AAA41103.1;
DR PIR; A38905; A38905.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PFO3028; Dynein_heavy; 1.
KM Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
FT DOMAIN 48 69
FT 179 200 COILED COIL (POTENTIAL).
FT DOMAIN 453 476 COILED COIL (POTENTIAL).
FT 541 564 COILED COIL (POTENTIAL).
FT DOMAIN 1169 1201 COILED COIL (POTENTIAL).
FT 1229 1250 COILED COIL (POTENTIAL).
FT DOMAIN 1355 1371 COILED COIL (POTENTIAL).
FT 2012 2040 COILED COIL (POTENTIAL).
FT DOMAIN 3187 3273 COILED COIL (POTENTIAL).
FT 3394 3498 COILED COIL (POTENTIAL).
FT DOMAIN 3735 3798 COILED COIL (POTENTIAL).
FT NP_BIND 2222 2229 ATP (POTENTIAL).
FT NP_BIND 2229 2229 ATP (POTENTIAL).

FT NP_BIND 2593 2600 ATP (POTENTIAL).
 FT NP_BIND 2935 2942 ATP (POTENTIAL).
 FT CONFLICT 1024 1025 SR -> MP (IN REF. 2).
 FT CONFLICT 1772 1772 N -> D (IN REF. 2).
 FT CONFLICT 2098 2098 P -> A (IN REF. 2).
 FT CONFLICT 2139 2139 F -> V (IN REF. 2).
 FT CONFLICT 2175 2175 D -> Q (IN REF. 2).
 FT CONFLICT 2185 2185 L -> V (IN REF. 2).
 FT CONFLICT 2366 2366 T -> S (IN REF. 2).
 FT CONFLICT 2382 2382 G -> A (IN REF. 2).
 FT CONFLICT 2463 2463 C -> D (IN REF. 2).
 FT CONFLICT 3219 3219 R -> K (IN REF. 2).
 FT CONFLICT 4131 4131 F -> S (IN REF. 2).
 FT CONFLICT 4366 4366 A -> G (IN REF. 2).
 FT CONFLICT 4511 4511
 SQ SEQUENCE 4644 AA; 532240 MM; 8C6ABDEB875D82 CRC64;

 Query Match 7.68; Score 98.5; DB 1; Length 4644;
 Best Local Similarity 23.58; Pred. No. 28;
 Matches 59; Conservative 32; Mismatches 83; Indels 77; Gaps 12;

 QY 53 LVLLHSVSSLSSELTETELKFLCGRVKKRLERVOGSL-----DL 93
 DB 376 LRLVFAISRLSSGLKVLGTRKIMHYAEEFEVWVACEVOTWDEYEKLVLRDI 435
 QY 94 FSMLEQN-----DLEPHTEL---IRELLASLRHDLR---RVDDFENGAAA---G 137
 DB 436 VKRRREENLKMVRINPAHRRKLRALDQMRKFRHQHQLRAVIVLRPQVTAVAQNOG 495
 QY 138 AARGEDLCA-----ENVICDNV---GKD-----WRRLAQLVSD 171
 DB 496 EAPPOOMKAEVLEPDAADANAIEVVAEENVEVDGLVSKGTEAME---AAMRYD 552
 QY 172 TKDISIDRYPRNTERESLRIRKNT-----EKENATVA---HLVGALRSCMNIVA 222
 DB 553 ERIDRYETR---ITALRROLGTRAKNANEMERFRFSFNLFPVPHIRGALREYQTLIQ 608
 QY 223 DLYOEVQOARD 233
 DB 609 RVKDDIESLHD 619

 RESULT 13
 HTR1_HALSA STANDARD; PRT; 535 AA.
 ID HTR1_HALSA
 AC P33955;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sensory rhodopsin I transducer (HTR-I) (Methyl-accepting phototaxis protein I) (MPP-I).
 GN HTR1 OR HTR1 OR HTR.
 OS Halobacterium salinarum.
 CC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 CC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID-2242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L33;
 RX MEDLINE-90384855; PubMed-2205842;
 RA Ferrando E., Kirsh M., Marwan W., Oesterhelt D.;
 RT "A gene from S. pombe with homology to E. coli RNase III blocks conjugation and sporulation when overexpressed in wild type cells";
 RL Nucleic Acids Res. 18:5304-5304(1990).
 RN [2]
 RP FUNCTION
 RX MEDLINE-94244615; PubMed-8187768;
 RA Kirsh M., Marwan W., Vermeglio A., Oesterhelt D.;
 RT "Phototaxis of Halobacterium salinarum requires a signalling complex of sensory rhodopsin I and its methyl-accepting transducer HtrI";
 RL EMO J. 13:2150-2155(1994).
 CC -I- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSOR RHODOPSIN I (SR-I) TO THE FLAGELLAR MOTOR. RESPONDS TO

CC
 CC -I- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSOR TRANSDUCERS FAMILY.
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 CC
 CC EMBL: X68591; CAA48578.1;
 DR PIR: S28466; S28466.
 DR HSSP: P02942; 1007.
 DR InterPro: IPR004089; Chmtaxis_transd.
 DR InterPro: IPR003660; HAMF.
 DR Pfam: PF00015; MCPsignal; 1.
 DR Pfam: PF00672; HAMF; 1.
 DR SMART: SM00304; HAMF; 2.
 DR SMART: SM00283; MA; 1.
 DR Transducer; Photoreceptor; Transmembrane; Methylation.
 KW INT_MET 0 8
 FT DOMAIN 1 8
 FT TRANSMEM 9 29
 FT DOMAIN 30 33
 FT TRANSMEM 34 34
 FT DOMAIN 35 53
 FT MOD_RES 265 265 POTENTIAL.
 FT MOD_RES 272 272 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 279 279 EXTRACELLULAR (POTENTIAL).
 FT MOD_RES 463 463 POTENTIAL.
 FT MOD_RES 472 472 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 535 AA; 56814 MM; 504A165A47FA8A5 CRC64;

 Query Match 7.48; Score 96.5; DB 1; Length 535;
 Best Local Similarity 23.68; Pred. No. 2.8;
 Matches 47; Conservative 37; Mismatches 64; Indels 51; Gaps 9;

 QY 88 QSGDLFMLEONDLEFGHTELLRELLASLRHDLRVD-----FEAGA 134
 DB 292 KSALDEMSITEVDPPGVGVEHLDQVAEIT--DIVDVTIDIEGTNMLALNASTAAR 349
 QY 135 AAGAARPEEDICAFNFTICNVGDMRRLAROLKVSPTKIDSIDRPRNTERESL- 193
 DB 350 AGNADDD---GEFVADEV-RD---LAEETQDRANEIAVAVEKTAQ--TEVTAASIO 399
 QY 194 ----RKMKTEKENATVAHLVGALRSCMNIVADVOEV-----QOARDLQNR 237
 DB 400 HTRIRVESGSETVSTILHT-----RTINDISIEVSNSIDEIGRTTSEQAETVOST 450
 QY 238 SGANSPMSWNSDASTSENS 256
 DB 451 ATSEYRVAGLSDDDTALAS 469

 RESULT 14
 RP54_PSEAE STANDARD; PRT; 497 AA.
 ID RP54_PSEAE
 AC P49988;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RNA polymerase sigma-54 factor.
 GN RPON OR PA4462.
 OS Pseudomonas aeruginosa.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID-287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PAK;
 RX MEDLINE-94156835; PubMed-8113171;
 RA Jin S., Ishimoto K., Lory S.;

FT	DISULEID	103	123	BY SIMILARITY.
FT	DISULEID	125	139	BY SIMILARITY.
FT	DISULEID	142	154	BY SIMILARITY.
FT	DISULEID	145	162	BY SIMILARITY.
FT	CARBOHYD	43	43	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	114	114	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	324 AA;	36835 MW;	D25D583C909D09 CRC64;

Query Match 7.2%; Score 93.5; DB 1; Length 324;
 Best Local Similarity 23.8%; Pred. No. 2.6;
 Matches 39; Conservative 26; Mismatches 68; Indels 31; Gaps 6;

OY	78	RVVKKRLERVOSGIDLFSSMLEQNDLEPGTELLRELLASLRHDLRRVDDFEAGAAG	137
Db	156	RTSNTCKCKROSSNYKILMLL-----ILPG-----LAILFVFTYKRYRKRPQDPESG----	202
OY	138	AARGEEDLCARFVYICDNGK-----DMRLAQLKYSDTKIDSIEDRYPRNL	185
Db	203	-IPSPESV--PMNVSDVNLNKYIWRTAERKKICDARKFARQHKIPESKIDIEHNSPDA	259
OY	186	TERVRESLRIMKTEKENATVAHLVGAIRSCQMLVADLVQEVQ	229
Db	260	AEQKIQLOQWYQSHGRTGACQALIGLRANR---CDIAEIQ	300

Search completed: June 19, 2003, 10:37:15
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:34:25 ; Search time 80 Seconds

(without alignments)
659.351 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNAQECRCRGSGILPGLGR.....RSGAMSPKMNNDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	716	55.0	208	11	Q8R2E7
2	131.5	10.1	482	11	Q9JHX4
3	128.5	9.9	476	13	Q918J3
4	128	9.8	538	4	Q8RDI5
5	125.5	9.6	480	11	Q89110
6	122.5	9.4	239	5	Q9V3B4
7	122	9.4	171	4	Q8RDI1
8	122	9.4	276	4	Q96R22
9	122	9.4	339	4	Q8RDI3
10	122	9.4	353	4	Q8RDI2
11	121.5	9.3	1856	4	Q99407
12	119.5	9.2	418	13	Q8RDI5
13	118.5	9.1	1719	4	Q13768
14	118	9.1	941	11	Q63128
15	117.5	9.0	1848	11	Q61302
16	116.5	8.9	1975	5	Q9VCD1

17	116	8.9	93	4	Q8RDI4	Q8td14 homo sapien
18	116	8.9	496	4	Q9COK4	Q9COK4 homo sapien
19	111	8.5	482	13	Q90WU1	Q90WU1 gallus gall.
20	110	8.4	462	4	Q96TE4	Q96TE4 homo sapien
21	109	8.4	520	13	Q9IB62	Q9IB62 xenopus lae
22	108	8.3	479	4	Q8RTO8	Q8RTO8 homo sapien
23	103.5	7.9	461	5	Q96407	Q96407 lltomopsis
24	103.5	7.9	970	5	Q17342	Q17342 caenorhabd1
25	103.5	7.9	985	5	Q17341	Q17341 caenorhabd1
26	103.5	7.9	1786	5	Q17344	Q17344 caenorhabd1
27	103	7.9	1809	5	Q17487	Q17487 caenorhabd1
28	103	7.9	1815	5	Q17488	Q17488 caenorhabd1
29	103	7.9	1867	5	Q17485	Q17485 caenorhabd1
30	103	7.9	2039	5	Q17489	Q17489 caenorhabd1
31	103	7.9	6994	5	Q17343	Q17343 caenorhabd1
32	101.5	7.8	500	13	Q9IB64	Q9IB64 xenopus lae
33	100	7.7	2091	5	Q9VJ69	Q9VJ69 drosophila
34	99.5	7.6	218	11	Q99M25	Q99M25 rattus norv
35	99	7.6	919	16	Q9RZ46	Q9RZ46 pseudomonas
36	99	7.6	927	2	Q87015	Q87015 pseudomonas
37	99	7.6	1955	5	Q61308	Q61308 parascaris
38	98	7.5	472	10	Q943N5	Q943N5 oryza sativ
39	97	7.5	487	5	Q9GNM2	Q9GNM2 stelya clav
40	97	7.5	622	17	Q9HQ32	Q9HQ32 halobacteri
41	97	7.5	665	4	Q96M89	Q96M89 homo sapien
42	96.5	7.4	560	4	Q8TB01	Q8TB01 homo sapien
43	96.5	7.4	1162	10	Q9LY65	Q9LY65 arabidopsis
44	96	7.4	647	16	Q9HUB1	Q9HUB1 pseudomonas
45	95.5	7.3	509	16	Q9A2N4	Q9A2N4 caulobacter

ALIGNMENTS

RESULT 1

Q8R2E7 PRELIMINARY; PRT; 208 AA.

AC Q8R2E7; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Fas death domain associated protein.

GN FADD.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.

OX NCBI_Taxid-10116;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE-ISCHEMIC BRAIN;

RA Spadoni C.G.;

RT Identification of neuronal caspases and involvement of death domain

RT proteins in neuronal apoptosis.

RL Thesis (2001), University of London, London, United Kingdom.

DR EMBL; AJ441127; CAD29628.1; -

SQ SEQUENCE 208 AA; 23124 MW; ABA3305406137CDB CRC64;

Query Match 55.0%; Score 716; DB 11; Length 208;

Best local Similarity 68.9%; Pred. No. 1.2e-51;

Matches 142; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

QY	49	MDPEVLHSSVSSSSSELTEIKFCLGRVYRKIERVQSGIDLFMSLIDNDLEPGHT	108
DB	1	MDPEVLHSSVSSSSSELTEIKFCLGRVYRKIERVQSGIDLFMSLIDNDLEPGHT	60
QY	109	ELIRELLASLRNDILRRVDDFAGAAAGAPGEELCAAFNYICNVGQDWRLAROLK	168
DB	61	GLIRELLASLRNDILRRVDDFAGAAAGAPGEELCAAFNYICNVGQDWRLAROLK	120

QY 169 VSDTKDISIEDRPRNTEREYRESURIKWTEKENATYAHVGLRSCOMLVADLVQEV 228
 DB 121 VSEAKIDIGIERRYSRSDRRETLRWKNEKENASVAGVYKALRACRLNVLVDLYVEA 180
 QY 229 QOARDLONRSGAMSPMSWNSDASTSE 254
 DB 181 LMAOGSVSKSDDTSSALRDSIVSFSE 206

RESULT 2

Q9JHX4 PRELIMINARY; PRT; 482 AA.
 AC Q9JHX4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Caspase-8.
 GN CASP8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Itch T., Itch A., Pleasure D.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-CEREBELLUM;
 RA Cao G., Graham S.H., Chen D., Chen J.;
 RT "Molecular cloning and characterization of rat caspase-8: its
 RT implication in delayed neuronal cell death after ischemia."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF279308; AAF87778.1;
 DR EMBL; AF288372; AAK83055.1;
 DR HSSP; Q15806; 10DU.
 DR MEROPS; C14.009;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

Query Match 10.1%; Score 131.5; DB 11; Length 482;
 Best Local Similarity 40.5%; Pred. No. 0.01;
 Matches 32; Conservative 12; Mismatches 34; Indels 1; Gaps 1;

QY 49 MDPFLVLLHSVSSLSSELTFLKFLCGRVYKRLLEVQSGDLFSMLLEQNDLEPGHT 108
 DB 1 MD-PRSCYDIAERLGNELALAKFLCDHLPKQESINDVLYLFQRLQEGMLEEDNL 59
 QY 109 ELRELASLRHDLRRV 127
 DB 60 SELKELFHISRDLRSRV 78

RESULT 3
 ID Q918J3 PRELIMINARY; PRT; 476 AA.
 AC Q918J3;
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=21927603; PubMed=11917123;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Caspase-8.
 GN CASP8.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in
 RT zebrafish."
 RL Cell Death Differ. 7:509-510(2000).
 DR EMBL; AF273220; AAF79207.1;
 DR HSSP; Q15806; 10DU.
 DR MEROPS; C14.009;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 SQ SEQUENCE 476 AA; 54890 MW; FD9DF4B3C3C1FB9 CRC64;

Query Match 9.9%; Score 128.5; DB 13; Length 476;
 Best Local Similarity 28.1%; Pred. No. 0.018;
 Matches 59; Conservative 29; Mismatches 83; Indels 39; Gaps 10;

QY 49 MDPFLVLLHSVSSLSSELTFLKFLCGRVYKRLLEVQSGDLFSMLLEQNDLEPGHT 108
 DB 1 MD-PRSCYDIAERLGNELALAKFLCDHLPKQESINDVLYLFQRLQEGMLEEDNL 55
 QY 109 ELRELASLRHDLRRVDFEAGAAAGAPGEDICAAFNVCNVGDD--WRRLA 164
 DB 56 ELLEPELLIAIGRIDLLEILKSKREV-----ERNL-----LNCDSRGSAYRRML 103
 QY 165 ROLKSDPKDISIEDR-----PRNTERVESLRWKTEKENA-----TVAHLVG 211
 DB 104 -LKISE--DWTENFPAKFLDLPPAKIGRSISFDALILEMKQRLPNDIDELR 158
 QY 212 ALRSCOMLVADLVQEVQOARDLONRSGAM 241
 DB 159 ILERCDKQLAVIERFRQSHNDQGGRL 188

RESULT 4
 ID Q8TD15 PRELIMINARY; PRT; 538 AA.
 AC Q8TD15;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Procaspase-8L.
 GN CASP8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=21927603; PubMed=11917123;

RA Breckenridge D.G., Nguyen M., Kupplig S., Reth M., Shore G.C.;
 RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
 RT complex at the endoplasmic reticulum.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
 DR EMBL: AF422925; AAL87628.1;
 SQ SEQUENCE 538 AA; 61863 MW; 54402ECFAC9F6C9 CRC64;
 Query Match 9.8%; Score 128; DB: 4; Length 538;
 Best Local Similarity 27.3%; Pred. No. 0.023; 70; Indels 32; Gaps 6;
 Matches 48; Conservative 26; Mismatches 70; Indels 32; Gaps 6;
 QY 17 LGRRLDARASPRTEGARRAPOPPLADPMDFELVY-----LHSYSSLSSETTEL 71
 DB 33 LGRRLDSEFAVPGKGG-----ADYLLPFKKMDPFRNLYDGEQDSEDLAST 81
 QY 72 KRLCLGRVYKRLERQSGDLDFSMLENDLEPHTLRLSLARHDL-----RR 126
 DB 82 KRLSLDYIPQRQEKIKALMLFORLQERMLEESNTSLFKELLRLINLLITYLNR 141
 QY 127 VDDFAGAAAGAPGEDICAFNYICDNVGRDWR-----LAROLKVSPTKID 175
 DB 142 KEEMEREL---QTPGRAQI-SAYRYALYQISEEVSRLSKRFLQSEISCKID 193
 RESULT 5
 089110 PRELIMINARY; PRT: 480 AA.
 AC 089110; 035669;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE CASPASE 8 precursor (EC 3.4.22.-) (CASPASE-8) (ICE-like apoptotic
 DE protease 5) (MORTI-associated CED-3 homolog) (MACH) (RAD-3-like
 DE ICE/CED-3-like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine
 DE protease) (Apoptotic protease MCH-5) (CAP4).
 GN CASP8 OR CASP-8 OR FLICE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-129/SV;
 RX MEDLINE-98316661; PubMed-9654089;
 RA Sakemai K., Tsukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8.";
 RT Eur. J. Biochem. 253:399-405(1998).
 RL [2]
 RL SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE-99057979; PubMed-9837723;
 RA Van de Craen M., Van Loc G., Declercq W., Schotte P.,
 RA Vandenabeele P.;
 RA "Molecular cloning and identification of murine caspase-8.";
 RT J. Mol. Biol. 284:1017-1026(1998).
 RL [3]
 RL SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RL SEQUENCE OF 57-476 FROM N.A.
 RA Submits P., Kischkel F., Poustka A., Kramer P.;
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
 CC TNF-1 INDUCED CELL DEATH. BINDING TO THE ADAPTER MOLECULE FADD
 CC RECRUITS IT TO EITHER RECEPTOR. THE RESULTING AGGREGATE CALLED THE
 CC DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
 CC LIBERATED FROM THE DISC AND ACTIVATES DOWNSTREAM APOPTOTIC
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIC
 CC (CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC. CLEAVES AND
 CC ACTIVATES CASPASE-1, -2, -3, -6, -7, -8, -11/4 AND -12.

CC -1- FUNCTION: MAY PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS.
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP).
 CC HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-1-AMC
 CC (BY SIMILARITY).
 CC -1- ENZYME REGULATION: INHIBITED BY 2-VAD-FK, CHMA AND P35.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC HIGHEST EXPRESSION IN HEART, THYMUS, LUNG, LIVER AND KIDNEY.
 CC LOWER EXPRESSION IN SPLEEN, THYMUS, LUNG, LIVER AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST EXPRESSION OCCURS AT
 CC DAY 7.
 CC -1- DOMAIN: CONTAINS TWO DEATH EFFECTOR DOMAINS (ALSO CALLED MORT
 CC MODULES) WHICH ARE INVOLVED IN THE BINDING OF CORRESPONDING
 CC SEQUENCE MOTIFS WITHIN FADD PROTEIN.
 CC -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE DISC
 CC WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC
 CC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND CASPASE-10 CAN
 CC BE INVOLVED IN THESE PROCESSING EVENTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
 CC CASPASE FAMILY.
 DR EMBL: AF067841; AAC40132.1;
 DR EMBL: AF067835; AAC40132.1; JOINED.
 DR EMBL: AF067836; AAC40132.1; JOINED.
 DR EMBL: AF067837; AAC40132.1; JOINED.
 DR EMBL: AF067838; AAC40132.1; JOINED.
 DR EMBL: AF067839; AAC40132.1; JOINED.
 DR EMBL: AF067840; AAC40132.1; JOINED.
 DR EMBL: AF067834; AAC40131.1;
 DR EMBL: AJ007749; CAAC07677.1;
 DR EMBL: AJ000641; CAAC04196.1;
 DR EMBL: BC006737; AAH06737.1;
 DR HSPB: O15806; 100D.
 DR MEROPS: C14.009;
 DR MGD: MG1:1261423; Casp8.
 DR InterPro: IPR001875; DEO.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF01335; DED; 2.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR SMART: SM00115; CASC; 1.
 DR SMART: SM00031; DED; 2.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR PROSITE: PS50168; DED; 2.
 KM Hydrolyase; Thiol protease; Apoptosis; zymogen.
 FT FT PROPEP 1 218
 FT CHAIN 1 218
 FT PROPEP 219 376
 FT PROPEP 377 387
 FT CHAIN 388 480
 FT ACT_SITE 319 319
 FT ACT_SITE 362 362
 FT DOMAIN 101 80
 FT DOMAIN 101 177
 FT CONFLICT 68 71
 FT CONFLICT 94 99
 FT CONFLICT 96 96
 FT CONFLICT 103 107
 FT CONFLICT 475 475
 FT CONFLICT 475 475
 SQ SEQUENCE 480 AA; 55356 MW; 045268AB3DE5E4F CRC64;
 Query Match 9.6%; Score 125.5; DB 11; Length 480;
 Best Local Similarity 39.5%; Pred. No. 0.032;
 Matches 30; Conservative 13; Mismatches 32; Indels 1; Gaps 1;
 QY 49 MDPEVLASVSSSSSELTELKRLGRVYKRLERQSGDLDFSMLENDLEPHT 108
 DB 1 MD-FOUCAIAMELESSEDLAKLFKCLDIDYIPHKQETLEDQKFLRLRKGMLEGN 59
 QY 109 ELLRELLASLRHDL 124

Db 60 SFLKELFHISRDLL 75

RESULT 6

AC 09V3B4 PRELIMINARY; PRT: 239 AA.

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)

DE C612397 protein (Death domain-containing adaptor protein).

GN Bg4 OR C612397.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_Taxid=7227;

RP SEQUENCE FROM N.A.

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Van K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Aroll J.F., Agbayani A., An H.-U., Andrews-Plankoch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evansgelist C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,

RA Jaitai M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Malsbina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Gibbs X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA "The genome sequence of Drosophila melanogaster."

RT Science 287:2185-2195(2000).

RL [2]

RP SEQUENCE FROM N.A.

RA Zhou L., Steller H.;

RT "Bg4, a potential Drosophila homologue of FAS-associated death-domain

RL containing protein (FADD).";

RL submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Hu S., Yang X.;

RP MEDLINE=20469420; PubMed=10934188;

RT "FADD, a Novel Death Domain-containing Adapter Protein for the

RL Drosophila Caspase DRSD."

RL J. Biol. Chem. 275:30761-30764(2000).

DR EMBL: AF003737; AAF55950.1;

DR EMBL: AF222005; AAF44325.1;

DR EMBL: AF295103; AAG22535.1;

DR FlyBase: FBgn0038928; Bg4.

DR InterPro: IPR000488; Death.

DR Pfam: PF00531; death; 1.

DR SMART: SM00005; DEATH; 1.

DR PROSITE: P550017; DEATH DOMAIN; 1.

SO SEQUENCE 239 AA; 27421 MW; F43CFMA546C3FCD9 CRC64;

Query Match 9.4%; Score 122.5; DB 5; Length 239;

Best Local Similarity 20.8%; Pred. No. 0.022;

Matches 46; Conservative 44; Mismatches 70; Indels 61; Gaps 7;

QY 65 SFLKELFHISRDLL-VKRLERVOGSLDFSLMLQNDLPHTLRELLSLR---120

DB 21 TENVEDLKLFVEISGRRSDCTRTEDLDCLERADESEYVEPLRISGMPOLE 80

QY 121 -----HDLRRVDFE-----AGAAAGAGGEDLCA-----148

DB 81 ALSATKPEITLGHVNLVYELALAEELRQQLAIPASQNAQPSVSLAAVPTAIQNY 140

QY 149 -----FNVCNDVGRKDMRLARQLKVSQTKIDSTEDRYPNLTERVRESLR 194

DB 141 ATPAAFTDHRKRTWFKKISELGRVYRRLGRSAGIGEGQDTIEERYPHDKSQI---LR 197

QY 195 IMKTEKENA-----YVAHLVGLRSCQMLVADLVQVEYQO 230

DB 198 LQQLIEDDCHDPKHFLLRLCRALGDCGRN---DLRRVQO 235

RESULT 7

AC 08TDL1 PRELIMINARY; PRT: 171 AA.

DT 01-JUN-2002 (TEMBLrel. 21, Created)

DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)

GN Procaspase-8 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=21927603; PubMed=11917123;

RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;

RT "The procaspase-8 isoform, procaspase-8L, recruited to the Bap31

RL complex at the endoplasmic reticulum."

RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).

DR EMBL: AF422929; AAL87632.1;

FT NON_TER 171 171

SO SEQUENCE 171 AA; 20361 MW; 5CBCA9EB5924CA9 CRC64;

Query Match 9.4%; Score 122; DB 4; Length 171;

Best Local Similarity 28.8%; Pred. No. 0.016;

Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

QY 56 LHSVSSLSSESTELKFLGLGRVKKRLERVOGSLDFSLMLQNDLPHTLRELL 115

DB 7 LYDIGEQLDSEDLASLKFSLDYTPQRKQEPIDALMLFQRLQEKRLSESNLSFLKEL 66

QY 116 ASLRRHDL-----RRYDDEAGAAAGAGGEDLCAAFVITCDNNGKDMRR-----L 163

DB 67 FRINRDLTLTYINTREKMEREL---QTGRRQI-SAYVMKYQISEEVSRLSFKF 122

QY 164 ARQLKVSQTKID 175

DB 123 LLOEISCKLID 134

RESULT 8

096722

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Query Match      9.4%; Score 123; DB 4; Length 276;
Best Local Similarity 28.8%; Pred. No. 0.03;
Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4

QY 56 LHSVSSLSSELTETLKEFLGKRVYRKLEKRVSGDLSFMLEQNDLEPGHTELLRELL 115
   | : : : : | | | | : : | : : : : | : : : : |
Db 7 LYDIEQGLDSEDLASTKFLSDIYIQKKEPFLKDALMLFQRLQEKRLMESNLSFLKELL 66
   | : : : : | | | | : : | : : : : | : : : : |

QY 116 ASLRHHLL-----RRVDDEAGAAAGAAGEEDLCAPENVICDNYGKIMR-----L 163
   | : : : : | | | | : : | : : : : | : : : : |
Db 67 FRINLDLLITYLNTRKEEMEREL--QTPGRAQI-SAYRYMLYQISEEVSSELSRKF 122
   | : : : : | | | | : : | : : : : | : : : : |

QY 164 ARQLKVPDPTKD 175
   | : : : : | | | | : : | : : : : |
Db 123 LLEQEISKCKLD 134
   | : : : : | | | | : : | : : : : |

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RESULT 9			
ID	Q8BD13	PRELIMINARY:	PRT; 339 AA.
AC	Q8BD13		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Procaspace-8 (Fragment).		
GN	CASP8.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21927603; PubMed=11917123;		
RA	Breckenridge D.G., Nguyen M., Kuppaly S., Reith M., Shore G.C.;		
RT	"The procaspase-8 isoform, procaspase-8L, recruited to the BAP31		
RL	complex at the endoplasmic reticulum."		
DR	Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).		
EMBL	AF422927; AAL87630.1; -.		
FT	NON_TER 339		
SQ	SEQUENCE 339 AA; 72PB2A620A5452B3 CR664;		

	Query Match	9.4%	Score 122	DB 4	length 339;	
	Best Local Similarity	28.8%	Pred. No. 0.039;			
	Matches	38;	Conservative	23;	Mismatches	55; Indels 16; Gaps 4
QY	56	LHSSVSSLSASSLTELKFLCGLRVYRKRLERVGSGIDLESMLEIIONDDEBGFHELLRELL	115			
		.: .				
Db	7	LYDIQEQLDSDELASTKFLSTLDYIPQRKEPPLTDALMLTQRQEKRYELSSNSISFKELL	66			

RESULT 10			
08DTD12			
ID	08DTD12	PRELIMINARY;	PRT; 353 AA.
AC	08DTD12;		
DT	01-JUN-2002 (TREMBLrel, 21, Created)		
DT	01-JUN-2002 (TREMBLrel, 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel, 21, Last annotation update)		
DE	Procaraspase-8 (Fragment).		
GN	CASP8.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21927603; PubMed=11917123;		
RA	Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;		
RT	"The procaspase-8 isoform, procaspase-8L, recruited to the Bap31		
RL	complex at the endoplasmic reticulum";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).		
DR	EMBL: AF429228; AAL87631.1; -.		
FT	NON_TTR		
SE	SEQUENCE 353 AA; 40905 MW; 797BB298A8354FC CRC64;		

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Query Match      9.48; Score 122; DB 4; Length 353;
Best Local Similarity 28.88; Pred. No. 0.041;
Matches 36; Conservative 23; Mismatches 55; Indels 16; Gaps 4

QY 56 LHSVSSLSSELTETELKFLGRVYRKRLERYQSGIDLFSLMLEQNDLEPHTELLRELL 115
   | : : : : | | | | : : | : : | | | | : : | : | |
Db 7 LYDIGEDLSEDDASLKNFLSDIYIPQRKEPIKDALMFLQRLEKRMEESSLFLELL 66
   | : : : : | | | | : : | : : | | | | : : | : | |

QY 116 ASLRHDDL-----RVVDPEAGAAAGAAPGEEDLCAPNYICDNGVGDNR-----L 165
   | : | | | : : : | : : | : : | : : | : : | : : |
Db 67 FRINRDLILTYITNTRKEEMEREL---QTPGRAQI-SAVRWALYQISEVSRSELSRSEK 122
   | : : : : | | | | : : | : : | : : | : : | : : |

QY 164 ARQLKYSDFKID 175
   | : : : : | : |
Db 123 LLOEISKCKID 134
   | : : : : | : |

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RESULT 11
099407 ID 099407 PRELIMINARY; PRT; 1856 AA.
AC 099407;
DT 01-MAY-1997 (TREMBLrel_03, Created)
DT 01-MAY-1997 (TREMBLrel_03, last sequence update)
DT 01-JUN-2002 (TREMBLrel_21, last annotation update)
DE Ankyrin.
GN ANK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP
RX MEDLINE=97382244; PubMed=9235914;
RA Gallaether P.G., Tse W.T., Scarpa A.L., Lux S.E., Forget B.G.;
RT "Structure and organization of the human ankyrin-1 gene. Basis for
RL complexity of pre-mRNA processing ";
J. Biol. Chem. 272:19220-19228(1997).
DR EMBL; U50133; AAB47805.1; -
DR EMBL; U50092; AAB47805.1; JOINED.
DR EMBL; U50093; AAB47805.1; JOINED.

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DR EMBL: U50094; AAB47805.1; JOINED.
DR EMBL: U50095; AAB47805.1; JOINED.
DR EMBL: U50096; AAB47805.1; JOINED.
DR EMBL: U50097; AAB47805.1; JOINED.
DR EMBL: U50098; AAB47805.1; JOINED.
DR EMBL: U50099; AAB47805.1; JOINED.
DR EMBL: U50100; AAB47805.1; JOINED.
DR EMBL: U50101; AAB47805.1; JOINED.
DR EMBL: U50102; AAB47805.1; JOINED.
DR EMBL: U50103; AAB47805.1; JOINED.
DR EMBL: U50104; AAB47805.1; JOINED.
DR EMBL: U50105; AAB47805.1; JOINED.
DR EMBL: U50106; AAB47805.1; JOINED.
DR EMBL: U50107; AAB47805.1; JOINED.
DR EMBL: U50108; AAB47805.1; JOINED.
DR EMBL: U50109; AAB47805.1; JOINED.
DR EMBL: U50110; AAB47805.1; JOINED.
DR EMBL: U50111; AAB47805.1; JOINED.
DR EMBL: U50112; AAB47805.1; JOINED.
DR EMBL: U50113; AAB47805.1; JOINED.
DR EMBL: U50114; AAB47805.1; JOINED.
DR EMBL: U50115; AAB47805.1; JOINED.
DR EMBL: U50116; AAB47805.1; JOINED.
DR EMBL: U50117; AAB47805.1; JOINED.
DR EMBL: U50118; AAB47805.1; JOINED.
DR EMBL: U50119; AAB47805.1; JOINED.
DR EMBL: U50120; AAB47805.1; JOINED.
DR EMBL: U50121; AAB47805.1; JOINED.
DR EMBL: U50122; AAB47805.1; JOINED.
DR EMBL: U50123; AAB47805.1; JOINED.
DR EMBL: U50124; AAB47805.1; JOINED.
DR EMBL: U50125; AAB47805.1; JOINED.
DR EMBL: U50126; AAB47805.1; JOINED.
DR EMBL: U50127; AAB47805.1; JOINED.
DR EMBL: U50128; AAB47805.1; JOINED.
DR EMBL: U50129; AAB47805.1; JOINED.
DR EMBL: U50130; AAB47805.1; JOINED.
DR EMBL: U50131; AAB47805.1; JOINED.
DR EMBL: U50132; AAB47805.1; JOINED.
DR HSSP: 000420; IAWC.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000906; ZUS.
DR Pfam: PF00023; ank; 23.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00791; ZUS; 1.
DR PRINTS: PR01415; ANKRYIN.
DR SMART: SM00248; ANK; 21.
DR SMART: SM00218; DEATH; 1.
DR SMART: SM00218; ZUS; 1.
DR PROSITE: PS50088; ANK_REPEAT; 20.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR ANK repeat: Repeat.
SQ SEQUENCE 1856 AA; 203466 MW; 4A4E3A794DD6401F CRC64;

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Query Match 9.3%; Score 121.5; DB 4; Length 1856;
Best Local Similarity 27.2%; Pred. No. 0.4;
Matches 34; Conservative 28; Mismatches 56; Indels -7; Gaps 2;

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QY 137 GAAGGEEEDICAAFNVICDNGVKDWKRLARQLKVSQTKSDTIEDRPRLTERVRESLRIM 196
DB 1370 GSLGTGEAEKMKAVISHGLSMAELARELOFVEDINRVRPNPLLSQSVALLIWM 1429
QY 197 KNTKENATVAHLVGLALSCOMLVADLVQ-EVQOARDLQ-----NRSGAMSPKSNMSD 249
DB 1430 VIRSGONAMNENTYALQSIDRGEIVNMLESGSGSRRLKFDRTDRDYSLSPQNMGY 1469
QY 250 ASTSE 254
DB 1490 SLIOD 1494

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RESULT 12
ID 08UVG5 PRELIMINARY; PRT; 418 AA.
AC 08UVG5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Claprl.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7953;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98021435; PubMed-9380701;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "Clarp, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis";
RT Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish";
RT Cell Death Differ. 7:509-510(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF448261; AAL41007.1;
DR InterPro: IPR001875; DED.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF01335; DED; 1.
DR SMART: SM00115; CASC; 1.
DR SMART: SM00031; DED; 2.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS50168; DED; 2.
SQ SEQUENCE 418 AA; 47619 MW; C2ECB3AE571E0237 CRC64;

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Query Match 9.2%; Score 119.5; DB 13; Length 418;
Best Local Similarity 25.6%; Pred. No. 0.083;
Matches 54; Conservative 35; Mismatches 83; Indels -39; Gaps 8;

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QY 2 NQAEPCREGGILGPL--GKRRDLA---ASEPRFGARRAGOPPLADPAMPDPLV 54
DB 53 NQAGPHSGNALLMELAMQMKRYDLKRVPTNQQVGIAR---KEVID-----YRV 104
QY 55 LHSVSSLSSELTELKFLCIGRVYKRLERVOGSLDLSMLLEQNDLEFGHTELLREL 114
DB 105 LMADVSEMDKEDLOSLIFLLSSILPKERSTRASFLDYVVELEKLNSEKIDFLKRC 164
QY 115 LASLRHDLRLRVDFEAGAAAGAEEDICAAFNVI-----CDNGKXMRRL----- 163
DB 165 LKNIRNDLVAKIQAYR-----NRGQNMCAAPNTKFTPMQCPPEKQVRSQCYNH 217
QY 164 --ARQLVSDTKI--DSIEDRYPRNLTER 188
DB 218 EFNRLKLSVPEPTGIHYQAITEEQMNEQR 248

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RESULT 13
ID 013768 PRELIMINARY; PRT; 1719 AA.
AC 013768;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Alt. ankyrin (variant 2.2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=HEMATOPOIETIC;
 MEDLINE=90158830; PubMed=2137557;
 RA Lux S.E., John K.M., Bennett V.;
 RT Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 structure with homology to tissue-differentiation and cell-cycle
 control proteins.
 RT Mature 344:36-42(1990).
 DR EMBL: X16603; CA34611.1;
 DR HSSP: Q00420; IAWC.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000906; ZUS.
 DR Pfam: PF00023; ank; 24.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00791; ZUS; 1.
 DR PRINTS: PRO1415; ANKYRIN.
 DR SMART: SM00248; ANK; 22.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00218; ZUS; 1.
 DR PROSITE: PS50086; ANK_REPEAT; 20.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW ANK repeat; Repeat.
 SO SEQUENCE 1719 AA; 189011 MW; F63465D16D975CBF CRC64;
 Query Match 9.18; Score 118.5; DB 4; Length 1719;
 Best Local Similarity 28.08; Pred. No. 0.64;
 Matches 33; Conservative 26; Mismatches 52; Indels 7; Gaps 2;
 OY 137 GAAPGEEDLCAAFNVICDNGKMDRRRLAROLKVSDFRTSDIEDRYPRNLTERRERESLRIV 196
 DB 1395 GSISGTEQAKMAKVAISEHGLSMAELARELOFSVEDINIRVENPNSLLEQSYALNTLM 1454
 OY 197 KNTKENATVAVHVGALRSQCNMLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWN 247
 DB 1455 VIREGQVANNENIYTLQSIDRGELVNMKGSGHQSRLNLPDRHRTRDYSLSFSQKN 1512
 RESULT 14
 ID 063128 PRELIMINARY; PRT; 941 AA.
 AC 063128;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Cpe2 protein.
 GN Cpe2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=HIPPOCAMPAL DENTATE GYRUS;
 RX MEDLINE=96312537; PubMed=8700883;
 RA Nedivi E., Fellous S., Theill L., Heyvoni D.;
 RT "A set of genes expressed in response to light in the adult cerebral
 cortex and regulated during development."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:2048-2053(1996).
 DR EMBL: X95466; CA64740.1;
 DR InterPro: IPR002017; Spectrin.
 SO SEQUENCE 941 AA; 109037 MW; EC50B042E22AF4248 CRC64;
 Query Match 9.18; Score 118; DB 11; Length 941;
 Best Local Similarity 22.78; Pred. No. 0.32;
 Matches 58; Conservative 47; Mismatches 96; Indels 54; Gaps 11;
 OY 11 GGLVPLGKRR---DLARSEPTEGARRAGQPRPADPMDPVLVLLHSVSSSSLS- 65

DB 678 GELLSMLKSLKRLIDVSSNE-----AQKRGDELAELSS-SKALVALLSEVEKMLSNF 731
 OY 66 SETLEKFLICIGVYKKEKTERVOG-----LDLSMLLEQNDLBERGHTELRE-----LIAS 117
 DB 732 GECVQK-----ELVSSLEGLMSGSESDENETIDTENTLEAQQMLLRHOKTMS 786
 OY 118 LRRHDLIRVYDVEGAGAGAPGEEDLCAAFNVICDNGKMDRRRLAROLKVSDFRTSDI 177
 DB 787 AKRRDLQOQEQGCGGQAG--PGQEL-----RKLESTLTGLDGS 825
 OY 178 EDRTYPRNLTERRERESLRIVKNTKENATVAVH-----GALRSQCNMLVADLVQEVQOAR 232
 DB 826 REQER---RIVYSLKMERFETNKETVAVYLFQGGSSHERLFSLSLSLEKOTK 881
 OY 233 DLNRSGAMSPMSWN 247
 DB 882 EFKRTESTINQOEN 896
 RESULT 15
 ID 061302 PRELIMINARY; PRT; 1848 AA.
 AC 061302;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Erythroid ankyrin.
 GN ANK1 OR ANK-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=NEURAL;
 RX MEDLINE=93252825; PubMed=848643;
 RA Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
 Barker J.E.;
 RT "Complex patterns of sequence variation and multiple 5' and 3' ends
 are found among transcripts of the erythroid ankyrin gene."
 RL J. Biol. Chem. 268:9533-9540(1993).
 DR EMBL: X69063; CA46801.1;
 DR HSSP: Q00420; IAWC.
 DR MGD: MGI:88024; ANK1.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000906; ZUS.
 DR Pfam: PF00023; ank; 24.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00791; ZUS; 1.
 DR PRINTS: PRO1415; ANKYRIN.
 DR SMART: SM00248; ANK; 22.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00218; ZUS; 1.
 DR PROSITE: PS50086; ANK_REPEAT; 20.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW ANK repeat; Repeat.
 SO SEQUENCE 1848 AA; 202577 MW; 5744BECBFEBA056 CRC64;
 Query Match 9.08; Score 117.5; DB 11; Length 1848;
 Best Local Similarity 27.98; Pred. No. 0.85;
 Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;
 OY 151 VICDNGKMDRRRLAROLKVSDFRTSDIEDRYPRNLTERRERESLRIVKNTKENATVAVH 210
 DB 1421 VIREHGLSMAELARELOFSVEDINIRVENPNSLLEQSYALNTLMVDRBENAKMENTLY 1480
 OY 211 GALSQCNMLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWDASTS 254
 DB 1481 TALNIDRSELVNLLEVSGHQSRLNLPDRHRTRDYSLSFSQKN 1531

Thu Jun 19 11:26:31 2003

Search completed: June 19, 2003, 10:38:43
Job time : 83 secs

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